WEST

Print Selection

Help | Clear | Cancel | Print | Print First Page

Select?	Document ID	Section(s)	Page(s)	# Pages to print	Database
☑	WO009937299A	all	all	* 51	JPAB,EPAB,DWPI
☑	WO000188103A	all	all	* 122	JPAB,EPAB,DWPI
☑	US006303301B	all	all	46	JPAB,EPAB,DWPI
☐	US006472154	all	all	* 588	USPT

Note: Print requests for more than **49** pages are denoted by '*' and are in red.

Building	Room	Printer
cm1	9e12	gbefptr

Main Menu | Logout

Generate Collection Print

L40: Entry 1 of 2 File: USPT Oct 29, 2002

DOCUMENT-IDENTIFIER: US 6472154 B1
TITLE: Polymorphic repeats in human genes

Detailed Description Paragraph Table (170):
L26953 3'UTR 4.16 2797 CAAAAA L27560 UNKNOWN 6 3438 GTT L27560 UNKNOWN 14 3658 A L27745 CDS 7 1067 AG L30117 UNKNOWN 79 652 T L31881 3'UTR 4.59 1481 CCCAG L32832 CDS 2.93 2092 GAGGAGGAGGAAGAA (SEQ ID NO:254) L32832 CDS 10 5866 CAA L32832 CDS 7.66 10261 CAG L32832 CDS 7 2985 GGC L33075 3'UTR 16 6723 A L33243 3'UTR 9 13947 TG L33477 3'UTR 10 3557 CA L34357 CDS 6 590 GGC L34408 UNKNOWN 15 706 A L35592 UNKNOWN 14 1577 AC L36140 5'UTR 24 1 T L36642 3'UTR 4 4333 CAAAA L36983 3'UTR 5.66 3368 CTC L37112 CDS 3.5 1257 CCTCAG L37198 UNKNOWN 23 7 A L38707 CDS 3.83 146 CCGGGG L38951 3'UTR 31 3653 A L38951 3'UTR 13 3736 T L38961 3'UTR 22 2283 T L39064 CDS 8.33 1504 AGC L39833 3'UTR 13 1809 A L39833 3'UTR 13 2713 T L40377 5'UTR 6.66 33 GCG L40377 5'UTR 6.33 51 GCA L40392 3'UTR 14 2209 T L40992 CDS 6 18 CAG L40992 BORDER 5.66 0 CAG L41690 CDS 6 620 GCC L41887 3'UTR 14 2046 A L41919 CDS 8 440 GGC L42025 5'UTR 5.66 1 GGC L42243 3'UTR 7 3934 GT L42243 3'UTR 16 2217 T L42243 3'UTR 15 1137 T L42243 3'UTR 12 2874 A L44505 UNKNOWN 13 309 A L46353 5'UTR 2.8 2094 CACACTCACA (SEQ ID NO:255) L46353 5'UTR 19 2401 TC L46353 5'UTR 9.5 2381 TC L46353 5'UTR 6.5 1394 TG L46353 5'UTR 13 264 A L46353 3'UTR 5 3378 TGGGG L48796 UNKNOWN 15 147 A L49169 3'UTR 6 1661 GAG L49169 3'UTR 6.5 2689 CT L49380 CDS 6 1771 GCC L76702 CDS 4.33 301 CAGCCC L76703 3'UTR 12 2219 A L77864 CDS 5.66 571 GAG L78833 3'UTR 18 6465 A M10901 3'UTR 18 3217 A M11220 3'UTR 5.5 693 TATT M11353 3'UTR 16 817 A M11722 5'UTR 14 216 G M12783 UNKNOWN 3.85 296 CGCAGCT M12783 UNKNOWN 7.5 3612 AC M12783 UNKNOWN 16 238 A M13232 3'UTR 6.5 1889 CA M13452 3'UTR 8.5 2030 GA M13452 3'UTR 15 1745 A M13903 CDS 5 528 GAGCAGCAGGAGGGGCAGCTGGAGCTCCCA (SEQ ID NO:256) M13903 CDS 3.43 679 AGCAGCAGGAGGGGCAGCTGGAGCTCTCTG (SEQ ID NO:257) M14058 3'UTR 12 2221 A M14083 3'UTR 7 2667 AT M14170 CDS 7.66 30 TGC M14219 3'UTR 13 1660 T M14630 UNKNOWN 12 538 A M14648 3'UTR 10.66 3535 TTG M14745 3'UTR 7.5 897 AC M14764 5'UTR 3.6 36 AGCGC M14764 3'UTR 7 2444 CA M15169 UNKNOWN 13 2852 C M15353 3'UTR 18 847 T M16276 UNKNOWN 12 1368 A M16505 UNKNOWN 6.5 2611 AC M16505 UNKNOWN 18 3645 A M16801 CDS 3.83 2295 CCCCCA M16937 3'UTR 2.7 865 AAACAAA (SEQ ID NO:258) M16938 5'UTR 7 172 TG M16965 CDS 2.94 115 TACCTTTGTTGGAAGACG (SEQ ID NO:259) M16965 CDS 2.5 591 CTGGAAGACATGGATTTT (SEQ ID NO:260) M18533 UNKNOWN 5.25 12297 TTGA M18533 UNKNOWN 8.5 11725 AC M18728 UNKNOWN 12 2266 A M19154 3'UTR 7.33 2117 ACA M19961 5'UTR 13 0 T M20681 UNKNOWN 13 2233 T M20681 UNKNOWN 13 3705 A M21305 CDS 6.4 56 TGGAA M21305 BORDER 3.8 0 ATGGA M21574 3'UTR 14 4503 T M23114 3'UTR 3.8 3839 CACCC M23263 CDS 20.33 1884 GGC M23263 CDS 17 701 GCA M24069 CDS 7.66 229 CCA M24283 3'UTR 9 2742 GT M24486 3'UTR 16 2350 T M24902 3'UTR 12.5 2338 AATA M25667 3'UTR 9 1153 CT M25667 3'UTR 17 973 A M28170 3'UTR 17 1816 GT M28713 5'UTR 6.66 253 CGG M29053 3'UTR 3.8 1579 AAAAT M29204 UNKNOWN 21 288 A M29873 3'UTR 6.5 1687 TA M29874 3'UTR 7 1688 AT M29874 3'UTR 15 2510 T M30448 3'UTR 26 887 A M31165 BORDER 12 900 A M31523 3'UTR 12 2316 T M31525 3'UTR 6.5 1037 AC M31682 3'UTR 8 1601 AG M31682 3'UTR 6.5 1886 TG M31732 3'UTR 15 1474 C M31899 CDS 5.66 869 GAA M31932 3'UTR 13 1430 T M32315 3'UTR 7.75 1814 TTTG M32315 3'UTR 6.5 3589 TG M32315 3'UTR 12 2368 A M34041 CDS 6.66 903 GAG M34309 5'UTR 6.S 4 CA M34539 3'UTR 12 1120 T M35531 3'UTR 6.25 2068 TTAT M35531 3'UTR 18 1752 T M35663 3'UTR 18 2056 T M36089 UNKNOWN 17 2462 AC M36542 3'UTR 18 1886 A M36711 3'UTR 6.66 1494 GCC M36820 3'UTR 6.25 540 TATT M36860 CDS 3.66 950 CAGCTG M37981 CDS 6.33 113 GCT M54915 5'UTR 3.8 246 CAGCA M54915 5'UTR 9 45 GCA M54915 3'UTR 5.25 2191 TATT M54927 3'UTR 14 2476 A M55047 3'UTR 22.5 2095 GT M55053 3'UTR 12 1915 T M55172 CDS 7.96 3238 CTGCCCCTGGAGTAGAGGACATCAGCGGGCTTCCTTCTG GAGAAGTTCTAGAGACCG (SEQ ID NO:261) M55172 CDS 5.52 2979 GGGCTTCCTTCTGGAGAAGTTCTAGAGACCACTGCCCCT GGAGTAGAGGACATCAGC (SEQ ID NO:262) M55172 CDS 5 3636 GCTGCCCCTGGAGTAGAGGACATCAGCGGGCTTCCTTCT GGAGAAGTTCTAGAGACT (SEQ ID NO:263) M55422 5'UTR 5.66 944 TTG M55542 3'UTR 14 2006 A M55593 5'UTR 7.33 87 GCG M55630 UNKNOWN 22 126 GT M55630 UNKNOWN 12 1538 A M55654 CDS 18.66 466 CAG M55654 CDS 9.66 430 CAG M55654 3'UTR 13 1297 T M55683 3'UTR 12 1203 TG M57627 3'UTR 3.5 1457 AAAAAT M58583 3'UTR 5.66 1354 TTG M59305 5'UTR 4.16 129 CTTTTT M59465 3'UTR 12 3986 A M59499 3'UTR 2.91 2093

TAGCTTCATGAA (SEQ ID NO:264) M59499 3'UTR 15 2248 T M59941 3'UTR 8 2912 AC M60052 CDS 14.33 911 GAT M60052 CDS 8.66 749 GAG M60314 5'UTR 13 637 T M60315 CDS 7 493 AGC M60626 3'UTR 13 1206 A M61108 3'UTR 12 3880 TG M61108 3'UTR 14 4060 T M61877 5'UTR 11.5 123 TC M61877 5'UTR 12 45 T M61877 3'UTR 17.5 7539 GT M62302 UNKNOWN 5.66 1799 GCG M62626 5'UTR 3.6 658 CCCCT M62831 3'UTR 4.75 1112 TTTG M63175 3'UTR 24 1503 T M64347 3'UTR 8 2317 TG M64347 3'UTR 6.5 2831 AT M64716 5'UTR 16 0 T M64930 UNKNOWN 14 3427 A M64936 UNKNOWN 50 3307 A M65131 UNKNOWN 28 2770 A M65290 3'UTR 4.75 2256 TTTA M68520 3'UTR 17 2047 T M69013 3'UTR 12 1386 T M73047 3'UTR 22 4250 T M73531 3'UTR 19 1757 T M73547 3'UTR 26.5 1412 AC M73746 CDS 5.66 73 GCT M74047 3'UTR 19 881 AT M74047 3'UTR 13 1966 T M74491 3'UTR 7 2744 TG M74491 3'UTR 6.5 1124 CT M74525 5'UTR 11.66 296 CGG M74525 5'UTR 12 381 T M74719 5'UTR 7.66 37 GGC M76558 CDS 3.5 2987 GGAAGA M76558 BORDER 7.66 509 GAT M76729 CDS 6.33 294 GCT M77140 3'UTR 12 461 T M77235 3'UTR 7 6773 CA M77498 CDS 3.73 447 GGTGGTTCTGGTGGT (SEQ ID NO:265) M77698 CDS 6 446 CCA M77698 CDS 5.66 366 GAG M77698 3'UTR 13 2018 A M77698 3'UTR 12 1641 A M80482 CDS 3.66 243 GGGCGCGGG M80899 3'UTR 7.5 3857 AT M81601 5'UTR 7.66 0 GCC M83216 CDS 3 1182 GGAGGAAGAGAAAAGGGCAGCAGAGGAGAGGCAGAGGAT AAA (SEQ ID NO:266) M83738 3'UTR 9 2798 TG M83751 CDS 8 256 GGA M84424 3'UTR 8.5 1341 AC M84739 5'UTR 14 25 C M85169 3'UTR 12 1712 T M85590 UNKNOWN 17 0 T M85670 UNKNOWN 13 227 A M86400 3'UTR 18 1632 T M86406 5'UTR 3.57 71 CGCCCGC M86406 3'UTR 6.5 2952 GA M86699 5'UTR 15 8 T M87503 CDS 7 574 AGC M87503 3'UTR 13 1400 T M88108 3'UTR 12 1749 A M88282 3'UTR 7.75 4728 AAAG M88282 3'UTR 16 4715 A M89796 3'UTR 23 2068 A M89796 3'UTR 14 1205 T M90391 CDS 6.66 694 CCT M90656 5'UTR 9.66 55 GGA M91463 3'UTR 23 2202 T

WEST Search History

DATE: Saturday, January 18, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=JPAB,EPAB,DWPI; PLUR=NO; OP=ADJ			
L44	L43 and (l27 or l26 or l25)	5	L44
L43	Golub[in[or Lander[in] or Pomeroy[in] or Tamayo[in]	441	L43
DB=USPT; PLUR=NO; OP=ADJ			
L42	L39 and l26	0	L42
L41	L39 and l27	0	L41
L40	M64347 or M64347?at	2	L40
L39	6303301[pn] or 6020135[pn]	2	L39
DB=JPAB,EPAB,DWPI; PLUR=NO; OP=ADJ			
L38	M64347 or M64347?at	0	L38
L37	L36 and M64347	0	L37
L36	6020135[pn]	1	L36
L35	L33 and M64347$2	0	L35
L34	L33 and M64347	0	L34
L33	6303301[pn]	1	L33
L32	L31 or l30	4	L32
L31	L29 and l27	1	L31
L30	L29 and l26	3	L30
L29	L28 or l25	78	L29
L28	cek2 or (cek adj 2)	0	L28
L27	(brain or cerebral or (choroid adj plexus) or cerebellum or hypothalmic) same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	4963	L27
L26	glioma$1 or glioblastoma$1 or medulloblastoma$1 or neurocytoma$1 or pinealoma$1 or astrocytoma$1 or ependymona$1 or craniopharyngioma$1	1273	L26
L25	FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor)	78	L25
DB=USPT; PLUR=NO; OP=ADJ			
L24	L20 and l15	0	L24
L23	L20 and l13	0	L23
L22	L20 and l10	0	L22
L21	L20 and l10	0	L21

L20	Golub[in[or Lander[in] or Pomeroy[in] or Tamayo[in]	234	L20
L19	L18 and l10	1	L19
L18	L17 or l16	343	L18
L17	L13[ti,ab]	251	L17
L16	L15[ti,ab]	105	L16
L15	glioma$1 or glioblastoma$1 or medulloblastoma$1 or neurocytoma$1 or pinealoma$1 or astrocytoma$1 or ependymona$1 or craniopharyngioma$1	3714	L15
L14	glioma$1 or glioblastoma$1 or medulloblastoma$1 or neurocytoma$1 or pinealoma$1 or astrocytoma$1 or ependy!mona$1 or craniopharyngioma$1	3714	L14
L13	(brain or cerebral or (choroid adj plexus) or cerebellum or hypothalmic) same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	9201	L13
L12	brain same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1)	8008	L12
L11	L10[ti.ab]	0	L11
L10	cek2 or (cek adj 2) or FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor adj (3 or III))	59	L10
L9	cek2 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	3	L9
L8	L7 and @ad<20010131	3	L8
L7	L6 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	3	L7
L6	cek or (cek adj (2 or II))	62	L6
L5	L4 or l3	16	L5
L4	L2 and @prad<20010131	6	L4
L3	L2 and @ad<20010131	14	L3
L2	L1 same (tumor$1 or tumour$1 or cancer$1 or cancerous or neoplas$3 or carcinoma$1 or teratoma$1 or papilloma$1 or glioma$1 or glioblastoma$1 or medulloblastoma$1)	16	L2
L1	FGFR3 or (FGF adj R3) or (fibroblast adj growth adj factor adj receptor adj (3 or III))	52	L1

END OF SEARCH HISTORY

WEST

Generate Collection Print

L5: Entry 11 of 16 File: USPT Apr 10, 2001

DOCUMENT-IDENTIFIER: US 6214795 B1
TITLE: Peptide compounds useful for modulating FGF receptor activity

DATE FILED (1):
19961112

Brief Summary Text (4):
The FGFs mediate their effects by binding to high affinity cell surface receptors (reviewed in Johnson and Williams (1992) Adv. Cancer Res. 60:1-41). Four distinct FGF receptors have been identified: FGFR1 (also known was Flg, bFGFR, Cek1 or N-bFGFR) (Lee et al. (1989) Science 245:57-60; Dionne et al. (1990) EMBO J. 9:2685-2692; Johnson et al. (1990) Mol. Cell. Biol. 10:4728-4736; Eisemann et al. (1991) Oncogene 6:1195-1202; Hou et al. (1991) Science 251:665-668), FGFR2 (also known as Bek, Cek3, K-sam, TK14, TK25 or KGFR) (Dionne et al. (1990) EMBO J. 9:2685-2692; Hattori et al. (1990) Proc. Natl. Acad. Sci. USA 87:5983-5987; Miki et al. (1991) Science 251:72-75; Saiki et al. (1988) Science 239:487-491; Pasquale (1990) Proc. Natl. Acad. Sci. USA 87:5812-5816; Houssaint et al. (1990) Proc. Natl. Acad. Sci. USA 87:8180-8184; Champion-Arnaud et al. (1991) Oncogene 6:979-987; Crumley et al. (1991) Oncogene 6:2255-2262; Raz et al. (1991) Oncogene 6:753-760; Sato et al. (1991) Oncogene 6:1279-1283), FGFR3 (also known as Cek2) (Keegan et al. (1991) Proc. Natl. Acad. Sci. USA 88:1095-1099) and FGFR4 (Partanen et al. (1991) EMBO J. 10:1347-1354).

6268391 + 6 more
6316479

Proc Natl Acad Sci U S A 1991 Feb 15;88(4):1095-9

Related Articles,

Links

Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3.

Keegan K, Johnson DE, Williams LT, Hayman MJ.

Department of Microbiology, State University of New York, Stony Brook 11794.

The fibroblast growth factors are a family of polypeptide growth factors involved in a variety of activities including mitogenesis, angiogenesis, and wound healing.

Fibroblast growth factor receptors (FGFRs) have previously been identified in chicken, mouse, and human and have been shown to contain an extracellular domain with either two or three immunoglobulin-like domains, a transmembrane domain, and a cytoplasmic tyrosine kinase domain. We have isolated a human cDNA for another tyrosine kinase receptor that is highly homologous to the previously described FGFR. Expression of this receptor cDNA in COS cells directs the expression of a 125-kDa glycoprotein. We demonstrate that this cDNA encodes a biologically active receptor by showing that human acidic and basic fibroblast growth factors activate this receptor as measured by 45Ca2+ efflux assays. These data establish the existence of an additional member of the FGFR family that we have named FGFR-3.

WEST

Generate Collection Print

L5: Entry 15 of 16 File: USPT Jul 21, 1998

DOCUMENT-IDENTIFIER: US 5783683 A
TITLE: Antisense oligonucleotides which reduce expression of the FGFRI gene

DATE FILED (1):
19950110

Drawing Description Text (10):
FIG. 9 shows an RT-PCR Southern Blot of FGFR1, FGFR3, and FGFR4 demonstrating the selective reduction of FGFR1 mRNA following treatment of glioblastoma cells with the antisense molecules of the invention.

Detailed Description Text (122):
mRNA was analyzed as described above with the exception that both FGFR1, FGFR3 and FGFR4 mRNA were studied in this particular work. SNB-19 glioblastoma cells were plated at 1.times.10.sup.5 cells per 100 mm dish in serum-supplemented medium. Eighteen hours later the cells were converted to serum-free medium containing FGFR1.alpha. antisense oligonucleotide (R1AS.alpha., 30 .mu.m) or FGFR1.alpha. antisense reverse control oligonucleotide (R1.alpha.RC, 30 .mu.m). Non-treated cells (NT) were run as a control. Cells were treated for three consecutive days with oligonucleotide. Cells were scraped on day 7 and mRNA and cDNA were purified and synthesized respectively. Using cDNA from each of the three different treatments, PCR was used to amplify cDNA for FGFR1, FGFR3, and FGFR4 receptors. SNB-19 cells do not produce FGFR2.

Gateway — your entrance to the knowledge resources of the National Library of Medicine

"Brain Neoplasms"[MESH] AND "Receptors, Fibroblast Growth Factor" [Search | Clear Search

Find Terms | Limits | Results | History | Locker | Preferences

New Search

Results

Overview
What's New
Help
FAQ

Other NLM Resources
Ordering Info.
Clinical Alerts
ClinicalTrials.gov
HSTAT
LOCATORplus
MEDLINEplus
PubMed
TOXNET

Journal Citations (2 collections searched)

Displaying items 1 - 20 of 25 found

Download or Display | Order Documents | Put in Locker | Deselect All

Page 1 of 2 Jump to Page 2 Jump to Collection Pick A Collection

1 ☐ Expand Related Articles

Subcellular localization of basic fibroblast growth factor and fibrobla growth factor receptor 1 in pituitary adenomas.
Fukui S, Otani N, Nawashiro H, Yano A, Nomura N, Miyazawa T, Ohnuk A, Tsuzuki N, Katoh H, Ishihara S, Shima K.
Brain Tumor Pathol. 2002;19(1):23-9.
PMID: 12455885 [PubMed - indexed for MEDLINE]
From PubMed

2 ☐ Expand Related Articles

Autocrine signaling through Ras regulates cell survival activity in hu glioma cells: potential cross-talk between Ras and the phosphatidylin 3-kinase-Akt pathway.
Sakata K, Kato S, Fox JC, Shigemori M, Morimatsu M.
J Neuropathol Exp Neurol. 2002 Nov;61(11):975-83.
PMID: 12430714 [PubMed - indexed for MEDLINE]
From PubMed

3 ☐ Expand Related Articles

Fibroblast growth factor receptor 4 is a target for the zinc-finger transcription factor Ikaros in the pituitary.
Yu S, Asa SL, Ezzat S.
Mol Endocrinol. 2002 May;16(5):1069-78.
PMID: 11981041 [PubMed - indexed for MEDLINE]
From PubMed

4 ☐ Expand Related Articles

Fibroblast growth factor receptor (FGFR) 4 correlated with the malignancy of human astrocytomas.
Yamada SM, Yamada S, Hayashi Y, Takahashi H, Teramoto A, Matsumc
Neurol Res. 2002 Apr;24(3):244-8.
PMID: 11958417 [PubMed - indexed for MEDLINE]
From PubMed

5 ☐ Expand Related Articles

Antitumor activity of fibroblast growth factors (FGFs) for medulloblastoma may correlate with FGF receptor expression and tu variant.
Duplan SM, Theoret Y, Kenigsberg RL.
Clin Cancer Res. 2002 Jan;8(1):246-57.

PMID: 11801566 [PubMed - indexed for MEDLINE]
From PubMed

6 ☐ Expand Related Articles
Targeted expression of a human pituitary tumor-derived isoform of F receptor-4 recapitulates pituitary tumorigenesis.
Ezzat S, Zheng L, Zhu XF, Wu GE, Asa SL.
J Clin Invest. 2002 Jan;109(1):69-78.
PMID: 11781352 [PubMed - indexed for MEDLINE]
From PubMed

7 ☐ Expand Related Articles
Pituitary adenomas in man and mouse: oncogenic potential of a trun fibroblast growth factor receptor 4.
Low MJ.
J Clin Invest. 2002 Jan;109(1):15-6. No Abstract Available.
PMID: 11781345 [PubMed - indexed for MEDLINE]
From PubMed

8 ☐ Expand Related Articles
Histological and genetic diagnosis of gliomatosis cerebri: case report.
Yamada SM, Hayashi Y, Takahashi H, Teramoto A, Matsumoto K, Yama
J Neurooncol. 2001 May;52(3):237-40.
PMID: 11519853 [PubMed - indexed for MEDLINE]
From PubMed

9 ☐ Expand Related Articles
Inhibition of fibroblast growth factor/fibroblast growth factor recept activity in glioma cells impedes tumor growth by both angiogenesis-dependent and -independent mechanisms.
Auguste P, Gursel DB, Lemiere S, Reimers D, Cuevas P, Carceller F, Di S JP, Bikfalvi A.
Cancer Res. 2001 Feb 15;61(4):1717-26.
PMID: 11245488 [PubMed - indexed for MEDLINE]
From PubMed

10 ☐ Expand Related Articles
Correlation of bFGF, FGFR-1 and VEGF expression with vascularity malignancy of human astrocytomas.
Bian XW, Du LL, Shi JQ, Cheng YS, Liu FX.
Anal Quant Cytol Histol. 2000 Jun;22(3):267-74.
PMID: 10872046 [PubMed - indexed for MEDLINE]
From PubMed

11 ☐ Expand Related Articles
Suppression of glioblastoma cell growth following antisense oligonucleotide-mediated inhibition of fibroblast growth factor recep expression.
Yamada SM, Yamaguchi F, Brown R, Berger MS, Morrison RS.
Glia. 1999 Oct;28(1):66-76.
PMID: 10498824 [PubMed - indexed for MEDLINE]
From PubMed

12 ☐ Expand Related Articles
[Inhibition of fibroblast growth factor receptor 1 expression in huma glioblastoma cell contributes to the cell growth suppression]
Yamada SM, Yamaguchi F, Morrison RS, Takahashi H, Teramoto A.
No To Shinkei. 1998 Dec;50(12):1101-5. Japanese.
PMID: 9989355 [PubMed - indexed for MEDLINE]
From PubMed

13 ☐ Expand Related Articles
Altered expression of fibroblast growth factor receptors in human pituitary adenomas.
Abbass SA, Asa SL, Ezzat S.
J Clin Endocrinol Metab. 1997 Apr;82(4):1160-6.
PMID: 9100589 [PubMed - indexed for MEDLINE]
From PubMed

14 ☐ Expand Related Articles
[Expression of fibroblast growth factor receptors (FGFRs) mRNA in human astrocytomas]
Yamada SM, Bruner JM, Berger MS, Morrison RS.
No To Shinkei. 1996 Apr;48(4):363-70. Japanese.
PMID: 8679334 [PubMed - indexed for MEDLINE]
From PubMed

15 ☐ Expand Related Articles
BK1: an FGF-responsive central nervous system-derived cell line.
Benvenisty N, Ornitz DM.
Growth Factors. 1995;12(1):49-55.
PMID: 8527163 [PubMed - indexed for MEDLINE]
From PubMed

16 ☐ Expand Related Articles
Transfection with bFGF sense and antisense cDNA resulting in modification of malignant glioma growth.
Redekop GJ, Naus CC.
J Neurosurg. 1995 Jan;82(1):83-90.
PMID: 7815139 [PubMed - indexed for MEDLINE]
From PubMed

17 ☐ Expand Related Articles
Enhanced expression of the tie receptor tyrosine kinase mesenger RN the vascular endothelium of metastatic melanomas.
Kaipainen A, Vlaykova T, Hatva E, Bohling T, Jekunen A, Pyrhonen S, A K.
Cancer Res. 1994 Dec 15;54(24):6571-7.
PMID: 7987857 [PubMed - indexed for MEDLINE]
From PubMed

18 ☐ Expand Related Articles
Immunohistochemical study for basic fibroblast growth factor and fibroblast growth factor receptor I in pituitary adenomas.
Suzui H, Takahashi JA, Fukumoto M, Hashimoto N, Itoh N, Hatanaka M, Kikuchi H.
Neurosci Lett. 1994 Apr 25;171(1-2):192-6.
PMID: 7916136 [PubMed - indexed for MEDLINE]
From PubMed

19 ☐ Expand Related Articles
Expression of fibroblast growth factor receptor-1 in human glioma ai meningioma tissues.
Ueba T, Takahashi JA, Fukumoto M, Ohta M, Ito N, Oda Y, Kikuchi H, Hatanaka M.
Neurosurgery. 1994 Feb;34(2):221-5; discussion 225-6.
PMID: 8177381 [PubMed - indexed for MEDLINE]
From PubMed

20 ☐ Expand Related Articles
Differential expression of two fibroblast growth factor-receptor genes associated with malignant progression in human astrocytomas.
Yamaguchi F, Saya H, Bruner JM, Morrison RS.
Proc Natl Acad Sci U S A. 1994 Jan 18;91(2):484-8.
PMID: 8290551 [PubMed - indexed for MEDLINE]

From PubMed

Journal Citations (2 collections searched)

Displaying items 1 - 20 of 25 found

Download or Display | Order Documents | Put in Locker | Deselect All

Page 1 of 2 

Jump to Page | 2 | Jump to Collection | Pick A Collection

Gateway
your entrance to the knowledge resources of the National Library of Medicine

"Brain Neoplasms"[MESH] AND "Receptors, Fibroblast Growth Factor"[Search Clear Search

Find Terms | Limits | Results | History | Locker | Preferences

New Search **Results**

Overview
What's New
Help
FAQ

Other NLM Resources
Ordering Info.
Clinical Alerts
ClinicalTrials.gov
HSTAT
LOCATORplus
MEDLINEplus
PubMed
TOXNET

Journal Citations (2 collections searched)

Displaying items 21 - 25 of 25 found

Download or Display | Order Documents | Put in Locker | Deselect All

Page 2 of 2 Jump to Page 1 Jump to Collection Pick A Collection

21 ☐ Expand Related Articles

Basic fibroblast growth factor and fibroblast growth factor receptor 1 implicated in the growth of human astrocytomas.
Morrison RS, Yamaguchi F, Saya H, Bruner JM, Yahanda AM, Donehow LA, Berger M.
J Neurooncol. 1994;18(3):207-16.
PMID: 7964981 [PubMed - indexed for MEDLINE]
From PubMed

22 ☐ Expand Related Articles

Identification and characterization of high molecular weight forms of basic fibroblast growth factor in human pituitary adenomas.
Li Y, Koga M, Kasayama S, Matsumoto K, Arita N, Hayakawa T, Sato B
J Clin Endocrinol Metab. 1992 Dec;75(6):1436-41.
PMID: 1464644 [PubMed - indexed for MEDLINE]
From PubMed

23 ☐ Expand Related Articles

Angiogenic activity of the K-fgf/hst oncogene in neural transplants.
Brustle O, Aguzzi A, Talarico D, Basilico C, Kleihues P, Wiestler OD.
Oncogene. 1992 Jun;7(6):1177-83.
PMID: 1375717 [PubMed - indexed for MEDLINE]
From PubMed

24 ☐ Expand Related Articles

Phosphorothioate antisense oligonucleotides against basic fibroblast growth factor inhibit anchorage-dependent and anchorage-independ growth of a malignant glioblastoma cell line.
Murphy PR, Sato Y, Knee RS.
Mol Endocrinol. 1992 Jun;6(6):877-84.
PMID: 1323055 [PubMed - indexed for MEDLINE]
From PubMed

25 ☐ Expand Related Articles

Gene expression of fibroblast growth factor receptors in the tissues of human gliomas and meningiomas.
Takahashi JA, Suzui H, Yasuda Y, Ito N, Ohta M, Jaye M, Fukumoto M, Y, Kikuchi H, Hatanaka M.
Biochem Biophys Res Commun. 1991 May 31;177(1):1-7.
PMID: 1645953 [PubMed - indexed for MEDLINE]
From PubMed

got I

Download or Display | Order Documents | Put in Locker | Deselect All

Journal Citations (2 collections searched)
Displaying items 21 - 25 of 25 found

M64347. Human novel growt...[gi:182564]

Links

```
LOCUS       HUMFGFLR                3829 bp    mRNA    linear   PRI 31-DEC-1994
DEFINITION  Human novel growth factor receptor mRNA, 3' cds.
ACCESSION   M64347
VERSION     M64347.1  GI:182564
KEYWORDS    growth factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3829)
  AUTHORS   Thompson,L.M., Plummer,S., Schalling,M., Altherr,M.R.,
            Gusella,J.F., Housman,D.E. and Wasmuth,J.J.
  TITLE     A gene encoding a fibroblast growth factor receptor isolated from
            the Huntington disease gene region of human chromosome 4
  JOURNAL   Genomics 11 (4), 1133-1142 (1991)
  MEDLINE   92147110
   PUBMED   1664411
COMMENT     Original source text: Homo sapiens cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1..3829
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="4p16.3 D4599"
     gene            1..3829
                     /gene="fgflr"
     CDS             <1..2196
                     /gene="fgflr"
                     /note="growth factor receptor"
                     /codon_start=1
                     /protein_id="AAA58470.1"
                     /db_xref="GI:182565"
                     /translation="KDGTGLVPSERVLVGPQRLQVLNASHEDSGAYSCRQRLTQRVLC
                     HFSVRVTDAPSSGDDEDGEDEAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCP
                     AAGNPTPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMESVVPSDRGNYTCVVENKFG
                     SIRQTYTLDVLERSPHRPILQAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEV
                     NGSKVGPDGTPYVTVLKTAGANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHS
                     AWLVVLPAEEELVEADEAGSVYAGILSYGVGFFLFILVVAAVTVCRLRSPPKKGLGSP
                     TVHKISRFPLKRQVSLESNASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWEL
                     SRARLTLGKPLGEGCFGQVVMAEAIGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSE
                     MEMMKMIGKHKNIINLLGACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCK
                     PPEEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVLVTEDNVMKIADFGLARD
                     VHNLDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIP
                     VEELFKLLKEGHRMDKPANCTHDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTVTST
                     DEYLDLSAPFEQYSPGGQDTPSSSSSGDDSVFAHDLLPPAPPSSGGSRT"
BASE COUNT      776 a   1100 c   1163 g    790 t
```

ORIGIN

```
       1 aaggatggca cagggctggt gccctcggag cgtgtcctgg tggggcccca gcggctgcag
      61 gtgctgaatg cctcccacga ggactccggg gcctacagct gccggcagcg gctcacgcag
     121 cgcgtactgt gccacttcag tgtgcgggtg acagacgctc catcctcggg agatgacgaa
     181 gacggggagg acgaggctga ggacacaggt gtggacacag gggcccctta ctggacacgg
     241 cccgagcgga tggacaagaa gctgctggcc gtgccggccg ccaacaccgt ccgcttccgc
     301 tgcccagccg ctggcaaccc cactccctcc atctcctggc tgaagaacgg cagggagttc
     361 cgcggcgagc accgcattgg aggcatcaag ctgcggcatc agcagtggag cctggtcatg
     421 gaaagcgtgg tgccctcgga ccgcggcaac tacacctgcg tcgtggagaa caagtttggc
     481 agcatccggc agacgtacac gctggacgtg ctggagcgct ccccgcaccg gcccatcctg
     541 caggcggggc tgccggccaa ccagacggcg gtgctgggca gcgacgtgga gttccactgc
     601 aaggtgtaca gtgacgcaca gccccacatc cagtggctca agcacgtgga ggtgaatggc
     661 agcaaggtgg gcccggacgg cacaccctac gttaccgtgc tcaagacggc gggcgctaac
     721 accaccgaca aggagctaga ggttctctcc ttgcacaacg tcacctttga ggacgccggg
     781 gagtacacct gcctggcggg caattctatt gggttttctc atcactctgc gtggctggtg
     841 gtgctgccag ccgaggagga gctggtggag gctgacgagg cgggcagtgt gtatgcaggc
     901 atcctcagct acggggtggg cttcttcctg ttcatcctgg tggtggcggc tgtgaccgtc
     961 tgccgcctgc gcagcccccc caagaaaggc ctgggctccc ccaccgtgca caagatctcc
    1021 cgcttcccgc tcaagcgaca ggtgtccctg gagtccaacg cgtccatgag ctccaacaca
    1081 ccactggtgc gcatcgcaag gctgtcctca ggggagggcc ccacgctggc caatgtctcc
    1141 gagctcgagc tgcctgccga ccccaaatgg gagctgtctc gggcccggct gaccctgggc
    1201 aagccccttg gggagggctg cttcggccag gtggtcatgg cggaggccat cggcattgac
    1261 aaggaccggg ccgccaagcc tgtcaccgta gccgtgaaga tgctgaaaga cgatgccact
    1321 gacaaggacc tgtcggacct ggtgtctgag atggagatga tgaagatgat cgggaaacac
    1381 aaaaacatca tcaacctgct gggcgcctgc acgcagggcg ggcccctgta cgtgctggtg
    1441 gagtacgcgg ccaagggtaa cctgcgggag tttctgcggg cgcggcggcc cccgggcctg
    1501 gactactcct tcgacacctg caagccgccc gaggagcagc tcaccttcaa ggacctggtg
    1561 tcctgtgcct accaggtggc ccggggcatg gagtacttgg cctcccagaa gtgcatccac
    1621 agggacctgg ctgcccgcaa tgtgctggtg accgaggaca acgtgatgaa gatcgcagac
    1681 ttcgggctgg cccgggacgt gcacaacctc gactactaca agaagacaac caacggccgg
    1741 ctccccgtga agtggatggc gcctgaggcc ttgtttgacc gagtctacac tcaccagagt
    1801 gacgtctggt cctttggggt cctgctctgg gagatcttca cgctgggggg ctccccgtac
    1861 cccggcatcc ctgtggagga gctcttcaag ctgctgaagg agggccaccg catggacaag
    1921 cccgccaact gcacacacga cctgtacatg atcatgcggg agtgctggca tgccgcgccc
    1981 tcccagaggc ccaccttcaa gcagctggtg gaggacctgg accgtgtcct taccgtgacg
    2041 tccaccgacg agtacctgga cctgtcggcg cctttcgagc agtactcccc gggtggccag
    2101 gacaccccca gctccagctc ctcaggggac gactccgtgt ttgcccacga cctgctgccc
    2161 ccggccccac ccagcagtgg gggctcgcgg acgtgaaggg ccactggtcc ccaacaatgt
    2221 gaggggtccc tagcagccca ccctgctgct ggtgcacagc cactccccgg catgagactc
    2281 agtgcagatg gagagacagc tacacagagc tttggtctgt gtgtgtgtgt gtgcgtgtgt
    2341 gtgtgtgtgt gcacatccgc gtgtgcctgt gtgcgtgcgc atcttgcctc caggtgcaga
    2401 ggtaccctgg gtgtccccgc tgctgtgcaa cggtctcctg actggtgctg cagcaccgag
    2461 gggcctttgt tctgggggga cccagtgcag aatgtaagtg ggcccacccg gtgggacccc
    2521 gtggggcagg gagctgggcc cgacatggct cggcctctgc ctttgcacca cgggacatca
    2581 cagggtgcgc tcggcccctc ccacacccaa agctgagcct gcagggaagc cccacatgtc
    2641 cagcaccttg tgcctggggt gttagtggca ccgcctcccc acctccaggc tttcccactt
    2701 cccaccctgc ccctcagaga ctgaaattac gggtacctga agatgggagc ctttaccttt
    2761 tatgcaaaag gtttattccg gaaactagtg tacatttcta taaatagatg ctgtgtatat
    2821 ggtatatata catatatata tataacatat atggaagagg aaaaggctgg tacaacggag
    2881 gcctgcgacc ctgggggcac aggaggcagg catggccctg ggcggggcgt ggggggcgt
```

```
2941 ggagggaggc cccaggggtc tcacccatgc aagcagagga ccagggcttt ttctggcacc
3001 gcagttttgt tttaaaactg gacctgtata tttgtaaagc tatttatggg cccctggcac
3061 tcttgttccc acaccccaac acttccagca tttagctggc cacatggcgg agagttttaa
3121 tttttaactt attgacaacc gagaaggttt atcccgccga tagagggacg gccaagaatg
3181 tacgtccagc ctgccccgga gctggaggat cccctccaag cctaaaaggt tgttaatagt
3241 tggaggtgat tccagtgaag atattttatt tgctttgtcc tttttcagga gaattagatt
3301 tctataggat ttttctttag gagatttatt ttttggactt caaagcaagc tggtattttc
3361 atacaaattc ttctaattgc tgtgtgtccc aggcagggag acggtttcca gggaggggcc
3421 ggccctgtgt gcaggttccg atgttattag atgttacaag tttatatata tctatatata
3481 taatttattg agtttttaca agatgtattt gttgtagact taacacttct tacgcaatgc
3541 ttctagagtt ttatagcctg gactgctacc tttcaaagct tggagggaag ccgtgaattc
3601 agttggttcg ttctgtactg ttactgggcc ctgagtctgg gcagctgtcc cttgcttgcc
3661 tgcagggcca tggctcaggg tggtctcttc ttggggccca gtgcatggtg gccagaggtg
3721 tcacccaaac cggcaggtgc gattttgtta acccagcgac gaactttccg aaaaataaag
3781 acacctggtt gctaacctga aaaaaaaaaa aaaaaaaaaa aaaaaaaaa
```

//

gi|182564|gb|M64347.1|HUMFGFLR Human novel growth factor receptor mRNA, 3' cds
Length = 3829

Score = 4551 bits (2296), Expect = 0.0
Identities = 2310/2317 (99%)
Strand = Plus / Plus

```
Query: 1    aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1    aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 60

Query: 61   gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 61   gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 120

Query: 121  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 180

Query: 181  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 181  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 240

Query: 241  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 241  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 300

Query: 301  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 360

Query: 361  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 361  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 420

Query: 421  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 421  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 480

Query: 481  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 481  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 540


Query: 541  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 600
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 541  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 600


Query: 601  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaatggc 660
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 601  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaatggc 660


Query: 661  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 661  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 720


Query: 721  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 780
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 721  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 780


Query: 781  gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 840
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 781  gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 840


Query: 841  gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 900
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 841  gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 900


Query: 901  atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgaccgtc 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 901  atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgaccgtc 960


Query: 961  tgccgcctgcgcagnnnnnnnaagaaaggcctgggctcccccaccgtgcacaagatctcc 1020
             ||||||||||||||       ||||||||||||||||||||||||||||||||||||||
Sbjct: 961  tgccgcctgcgcagcccccccaagaaaggcctgggctcccccaccgtgcacaagatctcc 1020


Query: 1021 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1021 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1080


Query: 1081 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 1081 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1140


Query: 1141 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1141 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1200


Query: 1201 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1201 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1260


Query: 1261 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1261 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1320


Query: 1321 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1321 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1380


Query: 1381 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1381 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1440


Query: 1441 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1441 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1500


Query: 1501 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1501 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1560


Query: 1561 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1561 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1620


Query: 1621 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1680
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1621 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1680


Query: 1681 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 1740
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Sbjct: 1681 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 1740


Query: 1741 ctccccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 1800
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1741 ctccccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 1800


Query: 1801 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1801 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 1860


Query: 1861 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1861 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 1920


Query: 1921 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1921 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 1980


Query: 1981 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1981 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2040


Query: 2041 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2041 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2100


Query: 2101 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2101 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2160


Query: 2161 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2161 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2220


Query: 2221 gaggggtccctagcagcccaccctgctgctggtgcacagccactccccggcatgagactc 2280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2221 gaggggtccctagcagcccaccctgctgctggtgcacagccactccccggcatgagactc 2280


Query: 2281 agtgcagatggagagacagctacacagagctttggtc 2317
            |||||||||||||||||||||||||||||||||||
```

```
Sbjct: 2281 agtgcagatggagagacagctacacagagctttggtc 2317
```

NM_000142. Homo sapiens fibr...[gi:13112046]

Links

LOCUS FGFR3 4093 bp mRNA linear PRI 21-FEB-2001
DEFINITION Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), transcript variant 1, mRNA.
ACCESSION NM_000142
VERSION NM_000142.2 GI:13112046
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4093)
AUTHORS Partanen,J., Makela,T.P., Alitalo,R., Lehvaslaiho,H. and Alitalo,K.
TITLE Putative tyrosine kinases expressed in K-562 human leukemia cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8913-8917 (1990)
MEDLINE 91062389
PUBMED 2247464
REFERENCE 2 (bases 1 to 4093)
AUTHORS Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
TITLE Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1095-1099 (1991)
MEDLINE 91142118
PUBMED 1847508
REFERENCE 3 (bases 1 to 4093)
AUTHORS Thompson,L.M., Plummer,S., Schalling,M., Altherr,M.R., Gusella,J.F., Housman,D.E. and Wasmuth,J.J.
TITLE A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4
JOURNAL Genomics 11 (4), 1133-1142 (1991)
MEDLINE 92147110
PUBMED 1664411
REFERENCE 4 (bases 1 to 4093)
AUTHORS Velinov,M., Slaugenhaupt,S.A., Stoilov,I., Scott,C.I. Jr., Gusella,J.F. and Tsipouras,P.
TITLE The gene for achondroplasia maps to the telomeric region of chromosome 4p
JOURNAL Nat. Genet. 6 (3), 314-317 (1994)
MEDLINE 94282083
PUBMED 8012397
REFERENCE 5 (bases 1 to 4093)
AUTHORS Le Merrer,M., Rousseau,F., Legeai-Mallet,L., Landais,J.C., Pelet,A., Bonaventure,J., Sanak,M., Weissenbach,J., Stoll,C., Munnich,A. et al.
TITLE A gene for achondroplasia-hypochondroplasia maps to chromosome 4p
JOURNAL Nat. Genet. 6 (3), 318-321 (1994)

MEDLINE 94282084
PUBMED 8012398
REFERENCE 6 (bases 1 to 4093)
AUTHORS Francomano,C.A., Ortiz de Luna,R.I., Hefferon,T.W., Bellus,G.A., Turner,C.E., Taylor,E., Meyers,D.A., Blanton,S.H., Murray,J.C., McIntosh,I. et al.
TITLE Localization of the achondroplasia gene to the distal 2.5 Mb of human chromosome 4p
JOURNAL Hum. Mol. Genet. 3 (5), 787-792 (1994)
MEDLINE 94362678
PUBMED 8081365
REFERENCE 7 (bases 1 to 4093)
AUTHORS Perez-Castro,A.V., Wilson,J. and Altherr,M.R.
TITLE Genomic organization of the human fibroblast growth factor receptor 3 (FGFR3) gene and comparative sequence analysis with the mouse Fgfr3 gene
JOURNAL Genomics 41 (1), 10-16 (1997)
MEDLINE 97271550
PUBMED 9126476
REFERENCE 8 (bases 1 to 4093)
AUTHORS Passos-Bueno,M.R., Wilcox,W.R., Jabs,E.W., Sertie,A.L., Alonso,L.G. and Kitoh,H.
TITLE Clinical spectrum of fibroblast growth factor receptor mutations
JOURNAL Hum. Mutat. 14 (2), 115-125 (1999)
MEDLINE 99355711
PUBMED 10425034
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from M58051.1 and M64347.1.
On Feb 23, 2001 this sequence version replaced gi:4503710.
Summary: The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Alternative splicing occurs and additional variants have been described, including those utilizing alternate exon 8 rather than 9, but their full-length nature has not been determined.
Transcript Variant: This variant (1) is missing alternatively spliced exon 8 but utilizes alternatively spliced exon 9, resulting in isoform (1) with the IIIc-type C-terminal half of the IgIII domain.

```
            COMPLETENESS: complete on the 3' end.
FEATURES             Location/Qualifiers
     source          1..4093
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4p16.3"
     gene            1..4093
                     /gene="FGFR3"
                     /note="synonyms: ACH, CEK2, JTK4"
                     /db_xref="LocusID:2261"
                     /db_xref="MIM:134934"
     CDS             40..2460
                     /gene="FGFR3"
                     /EC_number="2.7.1.112"
                     /note="isoform 1 is encoded by transcript variant 1;
                     protein-tyrosine kinase; tyrosylprotein kinase;
                     hydroxyaryl-protein kinase; human tyrosine kinase JTK4"
                     /codon_start=1
                     /product="fibroblast growth factor receptor 3, isoform 1
                     precursor"
                     /protein_id="NP_000133.1"
                     /db_xref="GI:4503711"
                     /db_xref="LocusID:2261"
                     /db_xref="MIM:134934"
                     /db_xref="MIM:134934"
                     /translation="MGAPACALALCVAVAIVAGASSESLGTEQRVVGRAAEVPGPEPG
                     QQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSERVLVGPQRLQVLNASHE
                     DSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGEDEAEDTGVDTGAPYWTRPERMD
                     KKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMESV
                     VPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPILQAGLPANQTAVLGSDVEFHCK
                     VYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKTAGANTTDKELEVLSLHNVTFEDA
                     GEYTCLAGNSIGFSHHSAWLVVLPAEEELVEADEAGSVYAGILSYGVGFFLFILVVAA
                     VTLCRLRSPPKKGLGSPTVHKISRFPLKRQVSLESNASMSSNTPLVRIARLSSGEGPT
                     LANVSELELPADPKWELSRARLTLGKPLGEGCFGQVVMAEAIGIDKDRAAKPVTVAVK
                     MLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVLVEYAAKGNLREF
                     LRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVL
                     VTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGV
                     LLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWHAAPSQRPT
                     FKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSSSSGDDSVFAHDLLPPAP
                     PSSGGSRT"
     sig_peptide     40..105
                     /gene="FGFR3"
     mat_peptide     106..2457
                     /gene="FGFR3"
                     /product="fibroblast growth factor receptor 3, isoform 1"
     misc_feature    199..369
                     /gene="FGFR3"
                     /note="IG; Region: Immunoglobulin"
                     /db_xref="CDD:IG"
```

```
misc_feature    547..744
                /gene="FGFR3"
                /note="IG; Region: Immunoglobulin"
                /db_xref="CDD:IG"
misc_feature    547..729
                /gene="FGFR3"
                /note="ig; Region: Immunoglobulin domain"
                /db_xref="CDD:pfam00047"
misc_feature    817..1098
                /gene="FGFR3"
                /note="IG_like; Region: Immunoglobulin like"
                /db_xref="CDD:IG_like"
misc_feature    841..1077
                /gene="FGFR3"
                /note="IG; Region: Immunoglobulin"
                /db_xref="CDD:IG"
misc_feature    841..1062
                /gene="FGFR3"
                /note="ig; Region: Immunoglobulin domain"
                /db_xref="CDD:pfam00047"
misc_feature    1453..2283
                /gene="FGFR3"
                /note="pkinase; Region: Eukaryotic protein kinase domain"
                /db_xref="CDD:pfam00069"
misc_feature    1453..2283
                /gene="FGFR3"
                /note="TyrKc; Region: Tyrosine kinase, catalytic domain"
                /db_xref="CDD:TyrKc"
misc_feature    1459..2286
                /gene="FGFR3"
                /note="S_TKc; Region: Serine/Threonine protein kinases,
                catalytic domain"
                /db_xref="CDD:S_TKc"
variation       232
                /gene="FGFR3"
                /allele="G"
                /allele="A"
                /db_xref="dbSNP:2305178"
misc_feature    969^970
                /gene="FGFR3"
                /note="Region: location of alternate exon 8"
misc_feature    970..1114
                /gene="FGFR3"
                /note="Region: alternate exon 9"
variation       1029
                /gene="FGFR3"
                /allele="T"
                /allele="C"
                /db_xref="dbSNP:2305185"
misc_feature    1115..1305
```

```
                     /gene="FGFR3"
                     /note="Region: alternate exon 10"
     variation       2496
                     /gene="FGFR3"
                     /allele="G"
                     /allele="A"
                     /db_xref="dbSNP:3135900"
     variation       2642
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:3135901"
     variation       2660
                     /gene="FGFR3"
                     /allele="G"
                     /allele="A"
                     /db_xref="dbSNP:3135902"
     variation       2977
                     /gene="FGFR3"
                     /allele="G"
                     /allele="C"
                     /db_xref="dbSNP:3135903"
     variation       3252
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:3135904"
     variation       3815
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:2121456"
     polyA_signal    4038..4043
                     /gene="FGFR3"
     polyA_site      4063
                     /gene="FGFR3"
                     /evidence=experimental
BASE COUNT      799 a   1198 c   1268 g    828 t
ORIGIN
        1 cgcgcgctgc ctgaggacgc cgcggccccc gcccccgcca tgggcgcccc tgcctgcgcc
       61 ctcgcgctct gcgtggccgt ggccatcgtg gccggcgcct cctcggagtc cttggggacg
      121 gagcagcgcg tcgtggggcg agcggcagaa gtcccgggcc cagagcccgg ccagcaggag
      181 cagttggtct tcggcagcgg ggatgctgtg gagctgagct gtcccccgcc cgggggtggt
      241 cccatggggc ccactgtctg ggtcaaggat ggcacagggc tggtgccctc ggagcgtgtc
      301 ctggtggggc cccagcggct gcaggtgctg aatgcctccc acgaggactc cggggcctac
      361 agctgccggc agcggctcac gcagcgcgta ctgtgccact tcagtgtgcg ggtgacagac
      421 gctccatcct cgggagatga cgaagacggg gaggacgagg ctgaggacac aggtgtggac
      481 acaggggccc cttactggac acggcccgag cggatggaca agaagctgct ggccgtgccg
      541 gccgccaaca ccgtccgctt ccgctgccca gccgctggca accccactcc ctccatctcc
      601 tggctgaaga acggcaggga gttccgcggc gagcaccgca ttggaggcat caagctgcgg
```

```
 661 catcagcagt ggagcctggt catggaaagc gtggtgccct cggaccgcgg caactacacc
 721 tgcgtcgtgg agaacaagtt tggcagcatc cggcagacgt acacgctgga cgtgctggag
 781 cgctccccgc accggcccat cctgcaggcg gggctgccgg ccaaccagac ggcggtgctg
 841 ggcagcgacg tggagttcca ctgcaaggtg tacagtgacg cacagcccca catccagtgg
 901 ctcaagcacg tggaggtgaa cggcagcaag gtgggcccgg acggcacacc ctacgttacc
 961 gtgctcaaga cggcgggcgc taacaccacc gacaaggagc tagaggttct ctccttgcac
1021 aacgtcacct ttgaggacgc cggggagtac acctgcctgg cgggcaattc tattgggttt
1081 tctcatcact ctgcgtggct ggtggtgctg ccagccgagg aggagctggt ggaggctgac
1141 gaggcgggca gtgtgtatgc aggcatcctc agctacgggg tgggcttctt cctgttcatc
1201 ctggtggtgg cggctgtgac gctctgccgc ctgcgcagcc cccccaagaa aggcctgggc
1261 tcccccaccg tgcacaagat ctcccgcttc ccgctcaagc gacaggtgtc cctggagtcc
1321 aacgcgtcca tgagctccaa cacaccactg gtgcgcatcg caaggctgtc ctcaggggag
1381 ggccccacgc tggccaatgt ctccgagctc gagctgcctg ccgaccccaa atgggagctg
1441 tctcgggccc ggctgaccct gggcaagccc cttggggagg gctgcttcgg ccaggtggtc
1501 atggcggagg ccatcggcat tgacaaggac cgggccgcca agcctgtcac cgtagccgtg
1561 aagatgctga aagacgatgc cactgacaag gacctgtcgg acctggtgtc tgagatggag
1621 atgatgaaga tgatcgggaa acacaaaaac atcatcaacc tgctgggcgc ctgcacgcag
1681 ggcgggcccc tgtacgtgct ggtggagtac gcggccaagg gtaacctgcg ggagtttctg
1741 cgggcgcggc ggcccccggg cctggactac tccttcgaca cctgcaagcc gcccgaggag
1801 cagctcacct tcaaggacct ggtgtcctgt gcctaccagg tggcccgggg catggagtac
1861 ttggcctccc agaagtgcat ccacagggac ctggctgccc gcaatgtgct ggtgaccgag
1921 gacaacgtga tgaagatcgc agacttcggg ctggcccggg acgtgcacaa cctcgactac
1981 tacaagaaga caaccaacgg ccggctgccc gtgaagtgga tggcgcctga ggccttgttt
2041 gaccgagtct acactcacca gagtgacgtc tggtcctttg gggtcctgct ctgggagatc
2101 ttcacgctgg ggggctcccc gtaccccggc atccctgtgg aggagctctt caagctgctg
2161 aaggagggcc accgcatgga caagcccgcc aactgcacac acgacctgta catgatcatg
2221 cgggagtgct ggcatgccgc gccctcccag aggcccacct tcaagcagct ggtggaggac
2281 ctggaccgtg tccttaccgt gacgtccacc gacgagtacc tggacctgtc ggcgcctttc
2341 gagcagtact ccccgggtgg ccaggacacc cccagctcca gctcctcagg ggacgactcc
2401 gtgtttgccc acgacctgct gcccccggcc ccacccagca gtgggggctc gcggacgtga
2461 agggccactg gtccccaaca atgtgagggg tccctagcag ccctccctgc tgctggtgca
2521 cagccactcc ccggcatgag actcagtgca gatggagaga cagctacaca gagctttggt
2581 ctgtgtgtgt gtgtgtgcgt gtgtgtgtgt gtgtgcacat ccgcgtgtgc ctgtgtgcgt
2641 gcgcatcttg cctccaggtg cagaggtacc ctgggtgtcc ccgctgctgt gcaacggtct
2701 cctgactggt gctgcagcac cgaggggcct ttgttctggg gggacccagt gcagaatgta
2761 agtgggccca cccggtggga ccccgtgggg cagggagctg ggcccgacat ggctcggcct
2821 ctgcctttgc accacgggac atcacagggt gcgctcggcc cctcccacac ccaaagctga
2881 gcctgcaggg aagccccaca tgtccagcac cttgtgcctg gggtgttagt ggcaccgcct
2941 ccccacctcc aggctttccc acttcccacc ctgcccctca gagactgaaa ttacgggtac
3001 ctgaagatgg gagcctttac cttttatgca aaaggtttat tccggaaact agtgtacatt
3061 tctataaata gatgctgtgt atatggtata tatacatata tatatataac atatatggaa
3121 gaggaaaagg ctggtacaac ggaggcctgc gaccctgggg gcacaggagg caggcatggc
3181 cctgggcggg gcgtgggggg gcgtggaggg aggccccagg ggtctcaccc atgcaagcag
3241 aggaccaggg ctttttctgg caccgcagtt ttgttttaaa actggacctg tatatttgta
3301 aagctattta tgggcccctg gcactcttgt tcccacaccc caacacttcc agcatttagc
3361 tggccacatg gcggagagtt ttaattttta acttattgac aaccgagaag gtttatcccg
3421 ccgatagagg gacggccaag aatgtacgtc cagcctgccc cggagctgga ggatcccctc
3481 caagcctaaa aggttgttaa tagttggagg tgattccagt gaagatattt tatttgcttt
3541 gtccttttc aggagaatta gatttctata ggatttttct ttaggagatt tatttttgg
3601 acttcaaagc aagctggtat tttcatacaa attcttctaa ttgctgtgtg tcccaggcag
```

```
3661 ggagacggtt tccagggagg ggccggccct gtgtgcaggt tccgatgtta ttagatgtta
3721 caagtttata tatatctata tatataattt attgagtttt tacaagatgt atttgttgta
3781 gacttaacac ttcttacgca atgcttctag agttttatag cctggactgc tacctttcaa
3841 agcttggagg gaagccgtga attcagttgg ttcgttctgt actgttactg ggccctgagt
3901 ctgggcagct gtcccttgct tgcctgcagg gccatggctc agggtggtct cttcttgggg
3961 cccagtgcat ggtggccaga ggtgtcaccc aaaccggcag gtgcgatttt gttaacccag
4021 cgacgaactt tccgaaaaat aaagacacct ggttgctaac ctgaaaaaaa aaaaaaaaaa
4081 aaaaaaaaaa aaa
```

gi|13112046|ref|NM_000142.2| Homo sapiens fibroblast growth factor receptor 3 (achondroplasia,
thanatophoric dwarfism) (FGFR3), transcript variant 1, mRNA
Length = 4093

Score = 4512 bits (2276), Expect = 0.0
Identities = 2305/2317 (99%)
Strand = Plus / Plus

```
Query: 1    aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 265  aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 324

Query: 61   gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 325  gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 384

Query: 121  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 385  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 444

Query: 181  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 445  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 504

Query: 241  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 505  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 564

Query: 301  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 565  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 624

Query: 361  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 625  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 684

Query: 421  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 685  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 744
```

```
Query: 481  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 745  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 804


Query: 541  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 805  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 864


Query: 601  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaatggc 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 865  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaacggc 924


Query: 661  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 925  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 984


Query: 721  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 985  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 1044


Query: 781  gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1045 gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 1104


Query: 841  gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1105 gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 1164


Query: 901  atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgaccgtc 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct: 1165 atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgacgctc 1224


Query: 961  tgccgcctgcgcagnnnnnnnaagaaaggcctgggctcccccaccgtgcacaagatctcc 1020
            |||||||||||||       ||||||||||||||||||||||||||||||||||||||
Sbjct: 1225 tgccgcctgcgcagcccccccaagaaaggcctgggctcccccaccgtgcacaagatctcc 1284


Query: 1021 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1285 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1344
```

```
Query: 1081 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1140
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1345 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1404


Query: 1141 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1405 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1464


Query: 1201 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1465 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1524


Query: 1261 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1525 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1584


Query: 1321 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1585 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1644


Query: 1381 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1440
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1645 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1704


Query: 1441 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1705 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1764


Query: 1501 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1560
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1765 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1824


Query: 1561 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1620
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1825 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1884


Query: 1621 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1680
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1885 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1944
```

```
Query: 1681 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 1740
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1945 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 2004


Query: 1741 ctccccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 1800
           || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2005 ctgcccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 2064


Query: 1801 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 1860
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2065 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 2124


Query: 1861 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 1920
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2125 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 2184


Query: 1921 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 1980
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2185 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 2244


Query: 1981 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2040
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2245 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2304


Query: 2041 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2100
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2305 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2364


Query: 2101 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2160
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2365 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2424


Query: 2161 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2220
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2425 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2484


Query: 2221 gaggggtccctagcagcccaccctgctgctggtgcacagccactccccggcatgagactc 2280
           |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct: 2485 gaggggtccctagcagccctccctgctgctggtgcacagccactccccggcatgagactc 2544
```

```
Query: 2281 agtgcagatggagagacagctacacagagctttggtc 2317
            |||||||||||||||||||||||||||||||||||||
Sbjct: 2545 agtgcagatggagagacagctacacagagctttggtc 2581
```

NM_022965. Homo sapiens fibr...[gi:13112047]

Links

LOCUS FGFR3 3757 bp mRNA linear PRI 21-FEB-2001
DEFINITION Homo sapiens fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism) (FGFR3), transcript variant 2, mRNA.
ACCESSION NM_022965
VERSION NM_022965.1 GI:13112047
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3757)
AUTHORS Partanen,J., Makela,T.P., Alitalo,R., Lehvaslaiho,H. and Alitalo,K.
TITLE Putative tyrosine kinases expressed in K-562 human leukemia cells
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 87 (22), 8913-8917 (1990)
MEDLINE 91062389
PUBMED 2247464
REFERENCE 2 (bases 1 to 3757)
AUTHORS Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
TITLE Isolation of an additional member of the fibroblast growth factor receptor family, FGFR-3
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1095-1099 (1991)
MEDLINE 91142118
PUBMED 1847508
REFERENCE 3 (bases 1 to 3757)
AUTHORS Thompson,L.M., Plummer,S., Schalling,M., Altherr,M.R., Gusella,J.F., Housman,D.E. and Wasmuth,J.J.
TITLE A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4
JOURNAL Genomics 11 (4), 1133-1142 (1991)
MEDLINE 92147110
PUBMED 1664411
REFERENCE 4 (bases 1 to 3757)
AUTHORS Velinov,M., Slaugenhaupt,S.A., Stoilov,I., Scott,C.I. Jr., Gusella,J.F. and Tsipouras,P.
TITLE The gene for achondroplasia maps to the telomeric region of chromosome 4p
JOURNAL Nat. Genet. 6 (3), 314-317 (1994)
MEDLINE 94282083
PUBMED 8012397
REFERENCE 5 (bases 1 to 3757)
AUTHORS Le Merrer,M., Rousseau,F., Legeai-Mallet,L., Landais,J.C., Pelet,A., Bonaventure,J., Sanak,M., Weissenbach,J., Stoll,C., Munnich,A. et al.
TITLE A gene for achondroplasia-hypochondroplasia maps to chromosome 4p
JOURNAL Nat. Genet. 6 (3), 318-321 (1994)

MEDLINE 94282084
PUBMED 8012398
REFERENCE 6 (bases 1 to 3757)
AUTHORS Francomano,C.A., Ortiz de Luna,R.I., Hefferon,T.W., Bellus,G.A., Turner,C.E., Taylor,E., Meyers,D.A., Blanton,S.H., Murray,J.C., McIntosh,I. et al.
TITLE Localization of the achondroplasia gene to the distal 2.5 Mb of human chromosome 4p
JOURNAL Hum. Mol. Genet. 3 (5), 787-792 (1994)
MEDLINE 94362678
PUBMED 8081365
REFERENCE 7 (bases 1 to 3757)
AUTHORS Perez-Castro,A.V., Wilson,J. and Altherr,M.R.
TITLE Genomic organization of the human fibroblast growth factor receptor 3 (FGFR3) gene and comparative sequence analysis with the mouse Fgfr3 gene
JOURNAL Genomics 41 (1), 10-16 (1997)
MEDLINE 97271550
PUBMED 9126476
REFERENCE 8 (bases 1 to 3757)
AUTHORS Passos-Bueno,M.R., Wilcox,W.R., Jabs,E.W., Sertie,A.L., Alonso,L.G. and Kitoh,H.
TITLE Clinical spectrum of fibroblast growth factor receptor mutations
JOURNAL Hum. Mutat. 14 (2), 115-125 (1999)
MEDLINE 99355711
PUBMED 10425034
COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The reference sequence was derived from AF245114.1 and M64347.1.
Summary: The protein encoded by this gene is a member of the fibroblast growth factor receptor family, where amino acid sequence is highly conserved between members and throughout evolution. FGFR family members differ from one another in their ligand affinities and tissue distribution. A full-length representative protein would consist of an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The extracellular portion of the protein interacts with fibroblast growth factors, setting in motion a cascade of downstream signals, ultimately influencing mitogenesis and differentiation. This particular family member binds acidic and basic fibroblast growth hormone and plays a role in bone development and maintenance. Mutations in this gene lead to craniosynostosis and multiple types of skeletal dysplasia. Alternative splicing occurs and additional variants have been described, including those utilizing alternate exon 8 rather than 9, but their full-length nature has not been determined.
Transcript Variant: This variant (2) does not contain alternatively spliced exons 8 or 9, resulting in a loss of the C-terminal half of the IgIII domain. In addition, this variant is missing alternatively spliced exon 10 which encodes the transmembrane region, suggesting a soluble receptor.

```
            COMPLETENESS: complete on the 3' end.
FEATURES             Location/Qualifiers
     source          1..3757
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4p16.3"
     gene            1..3757
                     /gene="FGFR3"
                     /note="synonyms: ACH, CEK2, JTK4"
                     /db_xref="LocusID:2261"
                     /db_xref="MIM:134934"
     CDS             40..2124
                     /gene="FGFR3"
                     /EC_number="2.7.1.112"
                     /note="isoform 2 is encoded by transcript variant 2;
                     protein-tyrosine kinase; tyrosylprotein kinase;
                     hydroxyaryl-protein kinase; human tyrosine kinase JTK4"
                     /codon_start=1
                     /product="fibroblast growth factor receptor 3, isoform 2
                     precursor"
                     /protein_id="NP_075254.1"
                     /db_xref="GI:13112048"
                     /db_xref="LocusID:2261"
                     /db_xref="MIM:134934"
                     /db_xref="MIM:134934"
                     /translation="MGAPACALALCVAVAIVAGASSESLGTEQRVVGRAAEVPGPEPG
                     QQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSERVLVGPQRLQVLNASHE
                     DSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGEDEAEDTGVDTGAPYWTRPERMD
                     KKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMESV
                     VPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPILQAGLPANQTAVLGSDVEFHCK
                     VYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKVSLESNASMSSNTPLVRIARLSSG
                     EGPTLANVSELELPADPKWELSRARLTLGKPLGEGCFGQVVMAEAIGIDKDRAAKPVT
                     VAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVLVEYAAKGN
                     LREFLRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAA
                     RNVLVTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVW
                     SFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWHAAPS
                     QRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSSSSGDDSVFAHDLL
                     PPAPPSSGGSRT"
     sig_peptide     40..105
                     /gene="FGFR3"
     mat_peptide     106..2121
                     /gene="FGFR3"
                     /product="fibroblast growth factor receptor 3, isoform 2"
     misc_feature    199..369
                     /gene="FGFR3"
                     /note="IG; Region: Immunoglobulin"
                     /db_xref="CDD:IG"
     misc_feature    547..744
                     /gene="FGFR3"
```

```
                     /note="IG; Region: Immunoglobulin"
                     /db_xref="CDD:IG"
     misc_feature    547..729
                     /gene="FGFR3"
                     /note="ig; Region: Immunoglobulin domain"
                     /db_xref="CDD:pfam00047"
     misc_feature    1117..1947
                     /gene="FGFR3"
                     /note="pkinase; Region: Eukaryotic protein kinase domain"
                     /db_xref="CDD:pfam00069"
     misc_feature    1117..1947
                     /gene="FGFR3"
                     /note="TyrKc; Region: Tyrosine kinase, catalytic domain"
                     /db_xref="CDD:TyrKc"
     misc_feature    1123..1950
                     /gene="FGFR3"
                     /note="S_TKc; Region: Serine/Threonine protein kinases,
                     catalytic domain"
                     /db_xref="CDD:S_TKc"
     variation       232
                     /gene="FGFR3"
                     /allele="G"
                     /allele="A"
                     /db_xref="dbSNP:2305178"
     variation       921
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:2234909"
     misc_feature    969^970
                     /gene="FGFR3"
                     /note="Region: location of alternate exons 8, 9, 10"
     variation       2160
                     /gene="FGFR3"
                     /allele="G"
                     /allele="A"
                     /db_xref="dbSNP:3135900"
     variation       2306
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:3135901"
     variation       2324
                     /gene="FGFR3"
                     /allele="G"
                     /allele="A"
                     /db_xref="dbSNP:3135902"
     variation       2641
                     /gene="FGFR3"
                     /allele="G"
```

```
                     /allele="C"
                     /db_xref="dbSNP:3135903"
     variation       2916
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:3135904"
     variation       3479
                     /gene="FGFR3"
                     /allele="T"
                     /allele="C"
                     /db_xref="dbSNP:2121456"
     polyA_signal    3702..3707
                     /gene="FGFR3"
     polyA_site      3727
                     /gene="FGFR3"
                     /evidence=experimental
BASE COUNT      744 a   1093 c   1160 g    760 t
ORIGIN
        1 cgcgcgctgc ctgaggacgc cgcggccccc gcccccgcca tgggcgcccc tgcctgcgcc
       61 ctcgcgctct gcgtggccgt ggccatcgtg gccggcgcct cctcggagtc cttggggacg
      121 gagcagcgcg tcgtggggcg agcggcagaa gtcccgggcc cagagcccgg ccagcaggag
      181 cagttggtct tcggcagcgg ggatgctgtg gagctgagct gtcccccgcc cgggggtggt
      241 cccatggggc ccactgtctg ggtcaaggat ggcacagggc tggtgccctc ggagcgtgtc
      301 ctggtggggc cccagcggct gcaggtgctg aatgcctccc acgaggactc cggggcctac
      361 agctgccggc agcggctcac gcagcgcgta ctgtgccact tcagtgtgcg ggtgacagac
      421 gctccatcct cgggagatga cgaagacggg gaggacgagg ctgaggacac aggtgtggac
      481 acaggggccc cttactggac acggcccgag cggatggaca agaagctgct ggccgtgccg
      541 gccgccaaca ccgtccgctt ccgctgccca gccgctggca accccactcc ctccatctcc
      601 tggctgaaga acggcaggga gttccgcggc gagcaccgca ttggaggcat caagctgcgg
      661 catcagcagt ggagcctggt catggaaagc gtggtgccct cggaccgcgg caactacacc
      721 tgcgtcgtgg agaacaagtt tggcagcatc cggcagacgt acacgctgga cgtgctggag
      781 cgctccccgc accggcccat cctgcaggcg gggctgccgg ccaaccagac ggcggtgctg
      841 ggcagcgacg tggagttcca ctgcaaggtg tacagtgacg cacagcccca catccagtgg
      901 ctcaagcacg tggaggtgaa cggcagcaag gtgggcccgg acggcacacc ctacgttacc
      961 gtgctcaagg tgtccctgga gtccaacgcg tccatgagct ccaacacacc actggtgcgc
     1021 atcgcaaggc tgtcctcagg ggagggcccc acgctggcca atgtctccga gctcgagctg
     1081 cctgccgacc ccaaatggga gctgtctcgg gcccggctga ccctgggcaa gccccttggg
     1141 gagggctgct tcggccaggt ggtcatggcg gaggccatcg gcattgacaa ggaccgggcc
     1201 gccaagcctg tcaccgtagc cgtgaagatg ctgaaagacg atgccactga caaggacctg
     1261 tcggacctgg tgtctgagat ggagatgatg aagatgatcg ggaaacacaa aaacatcatc
     1321 aacctgctgg gcgcctgcac gcagggcggg cccctgtacg tgctggtgga gtacgcggcc
     1381 aagggtaacc tgcgggagtt tctgcgggcg cggcggcccc cgggcctgga ctactccttc
     1441 gacacctgca agccgcccga ggagcagctc accttcaagg acctggtgtc ctgtgcctac
     1501 caggtggccc ggggcatgga gtacttggcc tcccagaagt gcatccacag ggacctggct
     1561 gcccgcaatg tgctggtgac cgaggacaac gtgatgaaga tcgcagactt cgggctggcc
     1621 cgggacgtgc acaacctcga ctactacaag aagacaacca acggccggct gcccgtgaag
     1681 tggatggcgc ctgaggcctt gtttgaccga gtctacactc accagagtga cgtctggtcc
     1741 tttggggtcc tgctctggga gatcttcacg ctgggggget ccccgtaccc cggcatccct
     1801 gtggaggagc tcttcaagct gctgaaggag ggccaccgca tggacaagcc cgccaactgc
```

1861 acacacgacc tgtacatgat catgcgggag tgctggcatg ccgcgccctc ccagaggccc
1921 accttcaagc agctggtgga ggacctggac cgtgtcctta ccgtgacgtc caccgacgag
1981 tacctggacc tgtcggcgcc tttcgagcag tactccccgg gtggccagga cacccccagc
2041 tccagctcct caggggacga ctccgtgttt gcccacgacc tgctgccccc ggccccaccc
2101 agcagtgggg gctcgcggac gtgaagggcc actggtcccc aacaatgtga ggggtcccta
2161 gcagccctcc ctgctgctgg tgcacagcca ctccccggca tgagactcag tgcagatgga
2221 gagacagcta cacagagctt tggtctgtgt gtgtgtgtgt gcgtgtgtgt gtgtgtgtgc
2281 acatccgcgt gtgcctgtgt gcgtgcgcat cttgcctcca ggtgcagagg taccctgggt
2341 gtccccgctg ctgtgcaacg gtctcctgac tggtgctgca gcaccgaggg gcctttgttc
2401 tgggggggacc cagtgcagaa tgtaagtggg cccacccggt gggaccccgt ggggcaggga
2461 gctgggcccg acatggctcg gcctctgcct ttgcaccacg ggacatcaca gggtgcgctc
2521 ggcccctccc acacccaaag ctgagcctgc agggaagccc cacatgtcca gcaccttgtg
2581 cctggggtgt tagtggcacc gcctccccac ctccaggctt tcccacttcc caccctgccc
2641 ctcagagact gaaattacgg gtacctgaag atgggagcct ttacctttta tgcaaaaggt
2701 ttattccgga aactagtgta catttctata aatagatgct gtgtatatgg tatatataca
2761 tatatatata taacatatat ggaagaggaa aaggctggta caacggaggc ctgcgaccct
2821 gggggcacag gaggcaggca tggccctggg cggggcgtgg gggggcgtgg agggaggccc
2881 caggggtctc acccatgcaa gcagaggacc agggcttttt ctggcaccgc agttttgttt
2941 taaaactgga cctgtatatt tgtaaagcta tttatgggcc cctggcactc ttgttcccac
3001 accccaacac ttccagcatt tagctggcca catggcggag agttttaatt tttaacttat
3061 tgacaaccga gaaggtttat cccgccgata gagggacggc caagaatgta cgtccagcct
3121 gccccggagc tggaggatcc cctccaagcc taaaaggttg ttaatagttg gaggtgattc
3181 cagtgaagat attttatttg ctttgtcctt tttcaggaga attagatttc tataggattt
3241 ttctttagga gatttatttt ttggacttca aagcaagctg gtattttcat acaaattctt
3301 ctaattgctg tgtgtcccag gcagggagac ggtttccagg gaggggccgg ccctgtgtgc
3361 aggttccgat gttattagat gttacaagtt tatatatatc tatatatata atttattgag
3421 tttttacaag atgtatttgt tgtagactta acacttctta cgcaatgctt ctagagtttt
3481 atagcctgga ctgctacctt tcaaagcttg gagggaagcc gtgaattcag ttggttcgtt
3541 ctgtactgtt actgggccct gagtctgggc agctgtccct tgcttgcctg cagggccatg
3601 gctcagggtg gtctcttctt ggggcccagt gcatggtggc cagaggtgtc acccaaaccg
3661 gcaggtgcga ttttgttaac ccagcgacga actttccgaa aaataaagac acctggttgc
3721 taacctgaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa

gi|13112047|ref|NM_022965.1| Homo sapiens fibroblast growth factor receptor 3 (achondroplasia,
thanatophoric dwarfism) (FGFR3), transcript variant 2, mRNA
Length = 3757

Score = 2518 bits (1270), Expect = 0.0
Identities = 1276/1278 (99%)
Strand = Plus / Plus

```
Query: 1040 aggtgtccctggagtccaacgcgtccatgagctccaacacaccactggtgcgcatcgcaa 1099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 968  aggtgtccctggagtccaacgcgtccatgagctccaacacaccactggtgcgcatcgcaa 1027


Query: 1100 ggctgtcctcaggggagggccccacgctggccaatgtctccgagctcgagctgcctgccg 1159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1028 ggctgtcctcaggggagggccccacgctggccaatgtctccgagctcgagctgcctgccg 1087


Query: 1160 accccaaatgggagctgtctcgggcccggctgaccctgggcaagccccttggggagggct 1219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1088 accccaaatgggagctgtctcgggcccggctgaccctgggcaagccccttggggagggct 1147


Query: 1220 gcttcggccaggtggtcatggcggaggccatcggcattgacaaggaccgggccgccaagc 1279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1148 gcttcggccaggtggtcatggcggaggccatcggcattgacaaggaccgggccgccaagc 1207


Query: 1280 ctgtcaccgtagccgtgaagatgctgaaagacgatgccactgacaaggacctgtcggacc 1339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1208 ctgtcaccgtagccgtgaagatgctgaaagacgatgccactgacaaggacctgtcggacc 1267


Query: 1340 tggtgtctgagatggagatgatgaagatgatcgggaaacacaaaaacatcatcaacctgc 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1268 tggtgtctgagatggagatgatgaagatgatcgggaaacacaaaaacatcatcaacctgc 1327


Query: 1400 tgggcgcctgcacgcagggcgggcccctgtacgtgctggtggagtacgcggccaagggta 1459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1328 tgggcgcctgcacgcagggcgggcccctgtacgtgctggtggagtacgcggccaagggta 1387


Query: 1460 acctgcgggagtttctgcgggcgcggcggcccccgggcctggactactccttcgacacct 1519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1388 acctgcgggagtttctgcgggcgcggcggcccccgggcctggactactccttcgacacct 1447
```

```
Query: 1520 gcaagccgcccgaggagcagctcaccttcaaggacctggtgtcctgtgcctaccaggtgg 1579
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1448 gcaagccgcccgaggagcagctcaccttcaaggacctggtgtcctgtgcctaccaggtgg 1507


Query: 1580 cccggggcatggagtacttggcctcccagaagtgcatccacagggacctggctgcccgca 1639
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1508 cccggggcatggagtacttggcctcccagaagtgcatccacagggacctggctgcccgca 1567


Query: 1640 atgtgctggtgaccgaggacaacgtgatgaagatcgcagacttcgggctggcccgggacg 1699
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1568 atgtgctggtgaccgaggacaacgtgatgaagatcgcagacttcgggctggcccgggacg 1627


Query: 1700 tgcacaacctcgactactacaagaagacaaccaacggccggctccccgtgaagtggatgg 1759
            |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct: 1628 tgcacaacctcgactactacaagaagacaaccaacggccggctgcccgtgaagtggatgg 1687


Query: 1760 cgcctgaggccttgtttgaccgagtctacactcaccagagtgacgtctggtcctttgggg 1819
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1688 cgcctgaggccttgtttgaccgagtctacactcaccagagtgacgtctggtcctttgggg 1747


Query: 1820 tcctgctctgggagatcttcacgctgggggctccccgtaccccggcatccctgtggagg 1879
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1748 tcctgctctgggagatcttcacgctgggggctccccgtaccccggcatccctgtggagg 1807


Query: 1880 agctcttcaagctgctgaaggagggccaccgcatggacaagcccgccaactgcacacacg 1939
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1808 agctcttcaagctgctgaaggagggccaccgcatggacaagcccgccaactgcacacacg 1867


Query: 1940 acctgtacatgatcatgcgggagtgctggcatgccgcgccctcccagaggcccaccttca 1999
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1868 acctgtacatgatcatgcgggagtgctggcatgccgcgccctcccagaggcccaccttca 1927


Query: 2000 agcagctggtggaggacctggaccgtgtccttaccgtgacgtccaccgacgagtacctgg 2059
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1928 agcagctggtggaggacctggaccgtgtccttaccgtgacgtccaccgacgagtacctgg 1987


Query: 2060 acctgtcggcgcctttcgagcagtactccccgggtggccaggacacccccagctccagct 2119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1988 acctgtcggcgcctttcgagcagtactccccgggtggccaggacacccccagctccagct 2047
```

```
Query: 2120 cctcaggggacgactccgtgtttgcccacgacctgctgcccccggccccacccagcagtg 2179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2048 cctcaggggacgactccgtgtttgcccacgacctgctgcccccggccccacccagcagtg 2107


Query: 2180 ggggctcgcggacgtgaagggccactggtccccaacaatgtgaggggtccctagcagccc 2239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2108 ggggctcgcggacgtgaagggccactggtccccaacaatgtgaggggtccctagcagccc 2167


Query: 2240 accctgctgctggtgcacagccactccccggcatgagactcagtgcagatggagagacag 2299
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2168 tccctgctgctggtgcacagccactccccggcatgagactcagtgcagatggagagacag 2227


Query: 2300 ctacacagagctttggtc 2317
            ||||||||||||||||||
Sbjct: 2228 ctacacagagctttggtc 2245
```

M58051. Human fibroblast ...[gi:182568]

Links

```
LOCUS       HUMFGFR3                2520 bp    mRNA    linear   PRI 08-NOV-1994
DEFINITION  Human fibroblast growth factor receptor (FGFR3) mRNA, complete cds.
ACCESSION   M58051
VERSION     M58051.1  GI:182568
KEYWORDS    fibroblast growth factor receptor.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2520)
  AUTHORS   Keegan,K., Johnson,D.E., Williams,L.T. and Hayman,M.J.
  TITLE     Isolation of an additional member of the fibroblast growth factor
            receptor family, FGFR-3
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1095-1099 (1991)
  MEDLINE   91142118
   PUBMED   1847508
COMMENT     Original source text: Human, cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1..2520
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /map="4p16.3"
                     /cell_line="CML K562"
     gene            1..2520
                     /gene="FGFR3"
     CDS             40..2460
                     /gene="FGFR3"
                     /codon_start=1
                     /product="fibroblast growth factor receptor"
                     /protein_id="AAA52450.1"
                     /db_xref="GI:182569"
                     /db_xref="GDB:G00-127-526"
                     /translation="MGAPACALALCVAVAIVAGASSESLGTEQRVVGRAAEVPGPEPG
                     QQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSERVLVGPQRLQVLNASHE
                     DSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGEDEAEDTGVDTGAPYWTRPERMD
                     KKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMESV
                     VPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPILQAGLPANQTAVLGSDVEFHCK
                     VYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKTAGANTTDKELEVLSLHNVTFEDA
                     GEYTCLAGNSIGFSHHSAWLVVLPAEEELVEADEAGSVYAGILSYGVGFFLFILVVAA
                     VTLCRLRSPPKKGLGSPTVHKISRFPLKRQVSLESNASMSSNTPLVRIARLSSGEGPT
                     LANVSELELPADPKWELSRARLTLGKPLGEGCFGQVVMAEAIGIDKDRAAKPVTVAVK
                     MLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVLVEYAAKGNLREF
                     LRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAARNVL
                     VTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVWSFGV
                     LLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWHAAPSQRPT
```

```
                     FKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSSSSGDDSVFAHDLLPPAP
                     PSSGGSRT"
     sig_peptide     40..105
                     /gene="FGFR3"
                     /note="G00-127-526"
     mat_peptide     106..2457
                     /gene="FGFR3"
                     /product="fibroblast growth factor receptor"
                     /note="G00-127-526"
BASE COUNT      441 a    827 c    840 g    412 t
ORIGIN
        1 cgcgcgctgc ctgaggacgc cgcggccccc gcccccgcca tgggcgcccc tgcctgcgcc
       61 ctcgcgctct gcgtggccgt ggccatcgtg gccggcgcct cctcggagtc cttggggacg
      121 gagcagcgcg tcgtggggcg agcggcagaa gtcccgggcc cagagcccgg ccagcaggag
      181 cagttggtct tcggcagcgg ggatgctgtg gagctgagct gtcccccgcc cgggggtggt
      241 cccatggggc ccactgtctg ggtcaaggat ggcacagggc tggtgccctc ggagcgtgtc
      301 ctggtggggc cccagcggct gcaggtgctg aatgcctccc acgaggactc cggggcctac
      361 agctgccggc agcggctcac gcagcgcgta ctgtgccact tcagtgtgcg ggtgacagac
      421 gctccatcct cgggagatga cgaagacggg gaggacgagg ctgaggacac aggtgtggac
      481 acaggggccc cttactggac acggcccgag cggatggaca agaagctgct ggccgtgccg
      541 gccgccaaca ccgtccgctt ccgctgccca gccgctggca accccactcc ctccatctcc
      601 tggctgaaga acggcaggga gttccgcggc gagcaccgca ttggaggcat caagctgcgg
      661 catcagcagt ggagcctggt catggaaagc gtggtgccct cggaccgcgg caactacacc
      721 tgcgtcgtgg agaacaagtt tggcagcatc cggcagacgt acacgctgga cgtgctggag
      781 cgctccccgc accggcccat cctgcaggcg gggctgccgg ccaaccagac ggcggtgctg
      841 ggcagcgacg tggagttcca ctgcaaggtg tacagtgacg cacagcccca catccagtgg
      901 ctcaagcacg tggaggtgaa cggcagcaag gtgggcccgg acggcacacc ctacgttacc
      961 gtgctcaaga cggcgggcgc taacaccacc gacaaggagc tagaggttct ctccttgcac
     1021 aacgtcacct ttgaggacgc cggggagtac acctgcctgg cgggcaattc tattgggttt
     1081 tctcatcact ctgcgtggct ggtggtgctg ccagccgagg aggagctggt ggaggctgac
     1141 gaggcgggca gtgtgtatgc aggcatcctc agctacgggg tgggcttctt cctgttcatc
     1201 ctggtggtgg cggctgtgac gctctgccgc ctgcgcagcc cccccaagaa aggcctgggc
     1261 tcccccaccg tgcacaagat ctcccgcttc ccgctcaagc gacaggtgtc cctggagtcc
     1321 aacgcgtcca tgagctccaa cacaccactg gtgcgcatcg caaggctgtc ctcaggggag
     1381 ggccccacgc tggccaatgt ctccgagctc gagctgcctg ccgaccccaa atgggagctg
     1441 tctcgggccc ggctgaccct gggcaagccc cttggggagg gctgcttcgg ccaggtggtc
     1501 atggcggagg ccatcggcat tgacaaggac cgggccgcca agcctgtcac cgtagccgtg
     1561 aagatgctga aagacgatgc cactgacaag gacctgtcgg acctggtgtc tgagatggag
     1621 atgatgaaga tgatcgggaa acacaaaaac atcatcaacc tgctgggcgc ctgcacgcag
     1681 ggcgggcccc tgtacgtgct ggtggagtac gcggccaagg gtaacctgcg ggagtttctg
     1741 cgggcgcggc ggcccccggg cctggactac tccttcgaca cctgcaagcc gcccgaggag
     1801 cagctcacct tcaaggacct ggtgtcctgt gcctaccagg tggcccgggg catggagtac
     1861 ttggcctccc agaagtgcat ccacagggac ctggctgccc gcaatgtgct ggtgaccgag
     1921 gacaacgtga tgaagatcgc agacttcggg ctggcccggg acgtgcacaa cctcgactac
     1981 tacaagaaga caaccaacgg ccggctgccc gtgaagtgga tggcgcctga ggccttgttt
     2041 gaccgagtct acactcacca gagtgacgtc tggtcctttg gggtcctgct ctgggagatc
     2101 ttcacgctgg ggggctcccc gtaccccggc atccctgtgg aggagctctt caagctgctg
     2161 aaggagggcc accgcatgga caagcccgcc aactgcacac acgacctgta catgatcatg
     2221 cgggagtgct ggcatgccgc gccctcccag aggcccacct tcaagcagct ggtggaggac
     2281 ctggaccgtg tccttaccgt gacgtccacc gacgagtacc tggacctgtc ggcgcctttc
```

```
2341 gagcagtact ccccgggtgg ccaggacacc cccagctcca gctcctcagg ggacgactcc
2401 gtgtttgccc acgacctgct gcccccggcc ccacccagca gtgggggctc gcggacgtga
2461 agggccactg gtccccaaca atgtgagggg tccctagcag ccctccctgc tgctggtgca
```

gi|182568|gb|M58051.1|HUMFGFR3 Human fibroblast growth factor receptor (FGFR3) mRNA, complete cds

Length = 2520

Score = 4391 bits (2215), Expect = 0.0
Identities = 2244/2256 (99%)
Strand = Plus / Plus

```
Query: 1    aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 265  aaggatggcacagggctggtgccctcggagcgtgtcctggtggggccccagcggctgcag 324


Query: 61   gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 325  gtgctgaatgcctcccacgaggactccggggcctacagctgccggcagcggctcacgcag 384


Query: 121  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 385  cgcgtactgtgccacttcagtgtgcgggtgacagacgctccatcctcgggagatgacgaa 444


Query: 181  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 445  gacggggaggacgaggctgaggacacaggtgtggacacaggggccccttactggacacgg 504


Query: 241  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 505  cccgagcggatggacaagaagctgctggccgtgccggccgccaacaccgtccgcttccgc 564


Query: 301  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 565  tgcccagccgctggcaaccccactccctccatctcctggctgaagaacggcagggagttc 624


Query: 361  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 625  cgcggcgagcaccgcattggaggcatcaagctgcggcatcagcagtggagcctggtcatg 684


Query: 421  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 685  gaaagcgtggtgccctcggaccgcggcaactacacctgcgtcgtggagaacaagtttggc 744


Query: 481  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 540
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 745  agcatccggcagacgtacacgctggacgtgctggagcgctccccgcaccggcccatcctg 804


Query: 541  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 805  caggcggggctgccggccaaccagacggcggtgctgggcagcgacgtggagttccactgc 864


Query: 601  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaatggc 660
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct: 865  aaggtgtacagtgacgcacagccccacatccagtggctcaagcacgtggaggtgaacggc 924


Query: 661  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 925  agcaaggtgggcccggacggcacaccctacgttaccgtgctcaagacggcgggcgctaac 984


Query: 721  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 985  accaccgacaaggagctagaggttctctccttgcacaacgtcacctttgaggacgccggg 1044


Query: 781  gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1045 gagtacacctgcctggcgggcaattctattgggttttctcatcactctgcgtggctggtg 1104


Query: 841  gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1105 gtgctgccagccgaggaggagctggtggaggctgacgaggcgggcagtgtgtatgcaggc 1164


Query: 901  atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgaccgtc 960
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  ||
Sbjct: 1165 atcctcagctacggggtgggcttcttcctgttcatcctggtggtggcggctgtgacgctc 1224


Query: 961  tgccgcctgcgcagnnnnnnnaagaaaggcctgggctccccccaccgtgcacaagatctcc 1020
            |||||||||||||       ||||||||||||||||||||||||||||||||||||||||
Sbjct: 1225 tgccgcctgcgcagcccccccaagaaaggcctgggctccccccaccgtgcacaagatctcc 1284


Query: 1021 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1080
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1285 cgcttcccgctcaagcgacaggtgtccctggagtccaacgcgtccatgagctccaacaca 1344


Query: 1081 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1140
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1345 ccactggtgcgcatcgcaaggctgtcctcaggggagggccccacgctggccaatgtctcc 1404


Query: 1141 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1405 gagctcgagctgcctgccgaccccaaatgggagctgtctcgggcccggctgaccctgggc 1464


Query: 1201 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1465 aagccccttggggagggctgcttcggccaggtggtcatggcggaggccatcggcattgac 1524


Query: 1261 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1525 aaggaccgggccgccaagcctgtcaccgtagccgtgaagatgctgaaagacgatgccact 1584


Query: 1321 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1585 gacaaggacctgtcggacctggtgtctgagatggagatgatgaagatgatcgggaaacac 1644


Query: 1381 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1645 aaaaacatcatcaacctgctgggcgcctgcacgcagggcgggcccctgtacgtgctggtg 1704


Query: 1441 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1705 gagtacgcggccaagggtaacctgcgggagtttctgcgggcgcggcggcccccgggcctg 1764


Query: 1501 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1765 gactactccttcgacacctgcaagccgcccgaggagcagctcaccttcaaggacctggtg 1824


Query: 1561 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1825 tcctgtgcctaccaggtggcccggggcatggagtacttggcctcccagaagtgcatccac 1884


Query: 1621 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1680
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1885 agggacctggctgcccgcaatgtgctggtgaccgaggacaacgtgatgaagatcgcagac 1944


Query: 1681 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 1740
```

```
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1945 ttcgggctggcccgggacgtgcacaacctcgactactacaagaagacaaccaacggccgg 2004


Query: 1741 ctccccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 1800
            || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2005 ctgcccgtgaagtggatggcgcctgaggccttgtttgaccgagtctacactcaccagagt 2064


Query: 1801 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 1860
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2065 gacgtctggtcctttggggtcctgctctgggagatcttcacgctgggggctccccgtac 2124


Query: 1861 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 1920
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2125 cccggcatccctgtggaggagctcttcaagctgctgaaggagggccaccgcatggacaag 2184


Query: 1921 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 1980
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2185 cccgccaactgcacacacgacctgtacatgatcatgcgggagtgctggcatgccgcgccc 2244


Query: 1981 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2040
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2245 tcccagaggcccaccttcaagcagctggtggaggacctggaccgtgtccttaccgtgacg 2304


Query: 2041 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2100
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2305 tccaccgacgagtacctggacctgtcggcgcctttcgagcagtactccccgggtggccag 2364


Query: 2101 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2160
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2365 gacacccccagctccagctcctcaggggacgactccgtgtttgcccacgacctgctgccc 2424


Query: 2161 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2425 ccggccccacccagcagtgggggctcgcggacgtgaagggccactggtccccaacaatgt 2484


Query: 2221 gaggggtccctagcagcccaccctgctgctggtgca 2256
            |||||||||||||||||| ||||||||||||||||
Sbjct: 2485 gaggggtccctagcagccctccctgctgctggtgca 2520
```

AF487554. Homo sapiens fibr...[gi:20452379]

Links

```
LOCUS       AF487554               16976 bp    DNA     linear   PRI 05-MAY-2002
DEFINITION  Homo sapiens fibroblast growth factor receptor 3 (FGFR3) gene,
            partial cds, alternatively spliced.
ACCESSION   AF487554
VERSION     AF487554.1  GI:20452379
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16976)
  AUTHORS   Lind,D.L. and Cox,D.R.
  TITLE     Fibroblast growth factor receptor 3 (FGFR3) genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 16976)
  AUTHORS   Lind,D.L. and Cox,D.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-FEB-2002) Genetics, Stanford University, SUMC M312,
            300 Pasteur Drive M/C 5120, Stanford, CA 94305-5120, USA
FEATURES             Location/Qualifiers
     source          1..16976
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4p16.3"
     gene            <1..>13026
                     /gene="FGFR3"
     mRNA            join(<5018..5287,5511..5576,7131..7300,7384..7507,
                     7599..7789,8678..8828,10094..10284,10588..10733,
                     11119..11240,11323..11433,11514..11704,11815..11937,
                     12021..12091,12310..12447,12593..12698,12880..>13026)
                     /gene="FGFR3"
                     /product="fibroblast growth factor receptor 3"
                     /note="alternatively spliced"
     mRNA            join(<5018..5287,5511..5576,7131..7300,7384..7507,
                     7599..7789,9456..9600,10094..10284,10588..10733,
                     11119..11240,11323..11433,11514..11704,11815..11937,
                     12021..12091,12310..12447,12593..12698,12880..>13026)
                     /gene="FGFR3"
                     /product="fibroblast growth factor receptor 3"
                     /note="alternatively spliced"
     CDS             join(<5018..5287,5511..5576,7131..7300,7384..7507,
                     7599..7789,8678..8828,10094..10284,10588..10733,
                     11119..11240,11323..11433,11514..11704,11815..11937,
                     12021..12091,12310..12447,12593..12698,12880..13026)
```

/gene="FGFR3"
/note="alternatively spliced"
/codon_start=3
/product="fibroblast growth factor receptor 3"
/protein_id="AAM22079.1"
/db_xref="GI:20452381"
/translation="VPGPEPGQQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGL
VPSERVLVGPQRLQVLNASHEDSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGED
EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRG
EHRIGGIKLRHQQWSLVMESVVPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPIL
QAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKSWI
SESVEADVRLRLANVSERDGGEYLCRATNFIGVAEKAFWLSVHGPRAAEEELVEADEA
GSVYAGILSYGVGFFLFILVVAAVTLCRLRSPPKKGLGSPTVHKISRFPLKRQVSLES
NASMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTLGKPLGEGCFGQ
VVMAEAIGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLG
ACTQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQV
ARGMEYLASQKCIHRDLAARNVLVTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVK
WMAPEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPA
NCTHDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQ
DTPSSSSSGDDSVFAHDLLPPAPPSSGGSRT"

CDS join(<5018..5287,5511..5576,7131..7300,7384..7507,
7599..7789,9456..9600,10094..10284,10588..10733,
11119..11240,11323..11433,11514..11704,11815..11937,
12021..12091,12310..12447,12593..12698,12880..13026)
/gene="FGFR3"
/note="alternatively spliced"
/codon_start=3
/product="fibroblast growth factor receptor 3"
/protein_id="AAM22078.1"
/db_xref="GI:20452380"
/translation="VPGPEPGQQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGL
VPSERVLVGPQRLQVLNASHEDSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGED
EAEDTGVDTGAPYWTRPERMDKKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRG
EHRIGGIKLRHQQWSLVMESVVPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPIL
QAGLPANQTAVLGSDVEFHCKVYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKTAG
ANTTDKELEVLSLHNVTFEDAGEYTCLAGNSIGFSHHSAWLVVLPAEEELVEADEAGS
VYAGILSYGVGFFLFILVVAAVTLCRLRSPPKKGLGSPTVHKISRFPLKRQVSLESNA
SMSSNTPLVRIARLSSGEGPTLANVSELELPADPKWELSRARLTLGKPLGEGCFGQVV
MAEAIGIDKDRAAKPVTVAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGAC
TQGGPLYVLVEYAAKGNLREFLRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVAR
GMEYLASQKCIHRDLAARNVLVTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVKWM
APEALFDRVYTHQSDVWSFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANC
THDLYMIMRECWHAAPSQRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDT
PSSSSSGDDSVFAHDLLPPAPPSSGGSRT"

exon 5018..5287
/gene="FGFR3"
/number=3

exon 5511..5576
/gene="FGFR3"
/number=4

```
     exon            7131..7300
                     /gene="FGFR3"
                     /number=5
     exon            7384..7507
                     /gene="FGFR3"
                     /number=6
     exon            7599..7789
                     /gene="FGFR3"
                     /number=7
     exon            8678..8828
                     /gene="FGFR3"
                     /note="alternatively spliced"
                     /number=8
     exon            9456..9600
                     /gene="FGFR3"
                     /note="alternatively spliced"
                     /number=9
     exon            10094..10284
                     /gene="FGFR3"
                     /number=10
     exon            10588..10733
                     /gene="FGFR3"
                     /number=11
     exon            11119..11240
                     /gene="FGFR3"
                     /number=12
     exon            11323..11433
                     /gene="FGFR3"
                     /number=13
     exon            11514..11704
                     /gene="FGFR3"
                     /number=14
     exon            11815..11937
                     /gene="FGFR3"
                     /number=15
     exon            12021..12091
                     /gene="FGFR3"
                     /number=16
     exon            12310..12447
                     /gene="FGFR3"
                     /number=17
     exon            12593..12698
                     /gene="FGFR3"
                     /number=18
     exon            12880..>13026
                     /gene="FGFR3"
                     /number=19
BASE COUNT     2747 a   5296 c   5682 g   3251 t
ORIGIN
        1 cagctaccct ccaagtgcga ggccaccacg gggagccagg ctgggggttg gcgtccgcag
```

```
  61 ccccgatccc ctgcgactcc ctagccctgg cctgtcggga gggcgcgggg ggccccattt
 121 ccacgattcc cgctgttgtt attcgggttc tgcgcagacg gaaagttccc attgttggcg
 181 tccccctccc ccgggcccca gtttgtggcc agcttcagcc aaggcgagag accggacttc
 241 taagggtggg tgtgcgcgtc agcgaagccc ggcccctgcc cgcccgaaga ggcagcagcc
 301 tccagcgtcc ccgctgccga ccctgccccc gcctgggggc cgagggcgct tccccgtggg
 361 tgcgcgccga gctccaggca agcgaggggc gcgtgtccca gcgtcgcggg ccctagactg
 421 ggctggcggt ccaggtcccg cgggacgtcg agggtctgaa gggaggtccc aaggggcgag
 481 gggaggggaa ggggcgcccg gccggacctg cacacgcgcc gcggttcctc gtgggccggg
 541 ccgagagctc cggtgccgcc gccgcgtaca cccgcagccg gctccggacg ggcgaggggg
 601 gcgcgcacag ctcagcccgg cggccgcgcg gagggaggcc ttggcccggt gagctcgcgc
 661 cccacccggg ccgaggcccg aacagccgct tctttgtacc tcgacgcggc cacagaccgc
 721 gcattgatgg cggctcggcg gctcgcgggg aggtgtgagc gaccgcgggc gcggcgggcc
 781 ggggagggcg cctggagggc cgaggcagat ggcgtccgcc ccgcccgcgc ccccgcgccc
 841 ctttctccgt cggcggctgc agcctcccgg aacaatgtca tttttttttat gaatgaaagt
 901 ggcccggcgc ttgaatgtgc gtgtcattca gcggcgtgac aggggccgtc gggaggtcag
 961 cgcgcgcttt tagcgtctgc tcgggcggcc ccgcttccag gggtgccgga ggggcggccg
1021 cgggggggagc ttggctttcg cattctcatt cagataaaga tattactccc tacggcccgg
1081 gaatgtcagc cagccccggg gaagggcggc ggccaggctg cggagcctct cctggacccc
1141 ctgcgggcgc gcggggcctc ccccagtcgc tcctggaacg ccccgcccac ccctcccccg
1201 gggcggcgcc cccgcccgca ctggagctgg tgaaacaggt agtgagttga tcggtcaata
1261 aacttaatcc ggttccttaa caagatgggc cgggcagtaa aaatacaaag acctcgtgaa
1321 atggactgag gtctaggctg gcgcttgccc gggaacataa attatggagc cttggctcgc
1381 aggggtcaag ggcggtggga aaggttttgg ccactggact gccctggcca ccccaggccc
1441 tgccaggaca gcccccatct ccccaggggg ccgtattcct ggttgggacc tggagtgacc
1501 ccccagggtg cagggaggta gacaaggtcg gctctcccac agtcccaccc cacccagcag
1561 gggtctgggg gtgcagggcc tttcccgaag gtgctggctg caacctcccc cactcctcct
1621 ctgcagggct ggactttgag ccgcgtgggc ctctgggtgg ttcattaacc tgggctgagc
1681 ctggcctcca ggtccttgtg tgagcctagg aaccccttgt tacccacccc ccagctcccc
1741 agccctcagg tctcacttgg ggctagatct ggggctgcgg cacccccttgt tacagctgag
1801 cttgagtggg agcccagggg cttggggtct cctggaggac ggggatctaa agtcacctca
1861 tctagggagg catgcagccc tcacctgagt gattcaggag tgaatgagcc aggagtggag
1921 ccacctttgg tggggtaggg gtcagcctgg acctctaggc tgccagctca ggctcgggtg
1981 ccctcttcga acctcagttt ccttacctgt ccaagagaac cgataatggc aggctgtttg
2041 aaggattagg ccagataacc ctggcaagcc ctctttagcc tgcccagcct ccagatccct
2101 tttttccgga ctttattgtg aaactccagg tggggagaca gggaggctgg acttttgggg
2161 gccccctcct cttaggctat tttatagctc ctacctggca atacctcctg taccccagag
2221 agctgcagag aacttcatgt gcatccgaaa ccagaatgtg ttgtttcctg accccaggcc
2281 ctcatctcac cccaaaaccc aaataaaccc ctggggcagc cagctccgga agcgagtctg
2341 gatttgatcc ttgttctctg gggtcaaccc gaggggctta tgatggagca aggctccccc
2401 atcctctcag ccatgctccc tcacatgcac tgggcctcca ctgcagagac ccagagcctg
2461 gagaaaggtt ccccaggcca gagtttggcc gtccccagca ccctgcctaa tggacatcag
2521 tcttggggcc agagacccag ggcagggagc gcctctcacc cctaccctca ctcctgcagc
2581 catttcaggg cctggtgccc tccctgagct cctgggcctg tggggtggga tttttacttt
2641 gtgccacagt gggggaaact gaggtacagg accagtgagt ggcagagttg tggagactct
2701 gggacacagc agagggctgt cgttggcatg tggagcccaa gttgaggtcg gcactgtgtg
2761 gggttggggc gccggcagga gcacgtgttg tgggatccat agaagggtgg gaggtgggac
2821 gcgttgcctc ctaccccgcc ttgggtacag caggagtttt gtctccaacg tgtttgggca
2881 ccagtgtctg tgtggtgtca gtggggcctc ccttttgtgg atcaagaaag aaagaaccct
2941 tcctagggct gctgggggggc tatagctctc cccatgcctg gcagctgggt ggggtatggg
3001 ggctccaccc aactgctgac ttcccagtgg gagtcagacc ctgaacttat agcacccact
```

3061 catgccccgt gtcacactgt ccttcacctg gtgctcgcca cccagcccct gctggggtac
3121 cctggcctct gctggcacct agcaggcagg cagtgggggg ggcagtcagg gctgcaccct
3181 ccccaccaca cacgggcaga tggccactgg tgtggctggc ctggggctgc tgtgtccccc
3241 gtccccccgt gctggaccag gctgaagcaa atacttgtgt ggatggcttg acctgttgtc
3301 gccactcaga ccaaaccgga accaaccggc tgttgccctt gggccagggc ctgcagctga
3361 ggctgccata accagcctgt tctcggcctt ctgggggggcc tcgagcagct cccagctctg
3421 ggtggtcccc acaagacact ggccaggacc ggagggctgg aggtcaggcc aggagccccc
3481 ctgactgcgg ggtccctaca ggggcagtcc ttgagctgtg ggtcccggtg gggcgagggc
3541 tccttcggat gcttcagggg atgagtgtgg gcccttctgg ctggcagggt caccctgggc
3601 actaggcgtg tgtggctgga tcaggtgggt tgggcagaag agggcctggc cgggcagcca
3661 gggactggtg tggccagagt gggcagctgg gcccccgaat ctaggccacg cgtctgcaga
3721 atgacaagtg atggcgcaac ccgcccagct gggtctgaag aaggaggctg cctgggggac
3781 cacccacccc cgtcccggcc ccaagcccgg gacgcctgcc tgcatgcatt gtctggccct
3841 ggcagggaag cctaggggcg attgtccccc cagccctgcc catggtgtgt ccttgggtca
3901 caggctttgg tggctctggg gagctgggca gctactgggg agggacccag gggccacctg
3961 cacatctgcc cctgtgggtg ggcccccacc ccagcttctc agcccccagg gaggggccag
4021 ggctgctgac ctgccctggc tctcacagct tcctgccccc agcctggtcg tcctctgtga
4081 gggggcccca gtccccctgc aggcagcagg actccacccc ccggcccct tgagggcccg
4141 cctgggcctc cccactcccc ggcctgtgag acccacttgg ccggacccag cgccgtgttt
4201 gtactttgct cttctcggta tgttttccgt catgaccgcc gtgtggagct tccataggag
4261 ctgcaggata cagaaccttg cccaccccaa ggagccccca cccccgcccc ggccccctcg
4321 cgctgctccg gcctgtgctc tgaccggtga acccgcgcat cgcccccag accgtccaca
4381 cggccacgtg accctgcacc tccttccttc tcgcctgttc tgttccctgg ctgtccatct
4441 gaactgcttt tcaggctcat atggggtgcg ggggctactg aggacggacc cctcctgggg
4501 tgaatctgca ccacgagggg gctggctggc caaccctggc acccccctctg agctccattt
4561 cagtcagagg ccagcaaagg gcagcctgtc ccctttgccc gcagcacctg cccgtcgtgg
4621 tgccgcctgt gagacaagca tggattttat gtttccaagc aattgaacaa attaaaagaa
4681 cgaagagtca cattttgtga cactttgaga tttgaattct ccgtgtccat gagtgaagca
4741 tcatggggcc actgctgtgg ggttggctgc aggttgtgtg gggaaggcgg ctgtcacacc
4801 gaggcagacc ggagtccttg ggacagactg gttggcaaag ctgaagatag agacctttgg
4861 ccctttgggg acacagtttc cagcccctgg tctggtggga ccctggatct gggtcagagc
4921 cttcctcact cagggccgcc gaggcttcca ctgctgtgtc tgtaaacggt gccgggtttg
4981 ggggtgcctg cctcatggtt gcccatcttc cccacagaag tcccgggccc agagcccggc
5041 cagcaggagc agttggtctt cggcagcggg gatgctgtgg agctgagctg tcccccgccc
5101 gggggtggtc ccatggggcc cactgtctgg gtcaaggatg gcacagggct ggtgccctcg
5161 gagcgtgtcc tggtggggcc ccagcggctg caggtgctga atgcctccca cgaggactcc
5221 ggggcctaca gctgccggca gcggctcacg cagcgcgtac tgtgccactt cagtgtgcgg
5281 gtgacaggtg agctctgggg ccacgccagc tacagaaagg agccgagtgc cgggctccct
5341 gagtccctgc gtgggtcagg agcggctggg ggtctctctg gtcattggtg gagaggaggg
5401 caccccccagg aagtgctgcc caaatggggg accctgcccc atctgggagg ggcacctggg
5461 ggcctcctgg ggcaggttgg gcattggttg cggccatctc tgccttgcag acgctccatc
5521 ctcgggagat gacgaagacg gggaggacga ggctgaggac acaggtgtgg acacaggtag
5581 gagcagggtc cagggttcag gccagccggg gtggggcccg ctgccaccgc caagccctgc
5641 ccttcacagg cagctgaggg actaaggccc cggaacaacc tccctggggt caccccgaag
5701 gtctggtccc ctcaggatac aggaggggct gggtcactga catggctcta gatgccccac
5761 cctggtggca gggctggggt gcaaggggac accgtgttgc tgatggggag actgaggcac
5821 agggccctgg gggttccagg agcaggagga ggccagggct ggcctgtggg gctctggtgt
5881 tggctatagg tgaggtggac cccgcagaca ttagcgcagc agggcagggc actcaggtgg
5941 ctgccgtggg gtggatggac ccggggtgag ggcgccgggg cacctgccac aaccagtggc
6001 gggcagggtg gctggcagga gggtggctgg tgggtgggct gcggctgtga gagagcagtc

6061 ggggacgatg cctggcgtcc cggcctggaa cggtggcagg tggactttgc caagttgtag
6121 ggtggggagg tggggcttct ggttttggag ggagctctga ggggagtgcg tgcaggtgag
6181 ggtcatcgtg gcacagacat ggggggcagt tacgacttgc ggactgatgg tgtgtgcgct
6241 gggtccctgg gccagtgggg taagcaggtg aggaagggag gctgagtcca tgagagaaac
6301 agctggggga actcaccctg ggggtctcca ggaggcctgg gagggagctc agcaccgtgg
6361 ggtgcctctt tccagcctgt gtccacactg ctgcttgctg ggcctcagtg cccctgatgg
6421 gcgtgtgcct ggaggggggct ggcagtgagc tcactgaggg gagggctgct tccctcctgg
6481 ggaatgccag cccatccttg cctggagtcc cggcaggaag gcagcaccag ccctgaggaa
6541 ggagaaaaac cagttgggct gtgagagggg tggtgggagc cctggacatc gagatgggag
6601 gaggcagggc ctccagggtg ccaccgtctc tgggtgcccg ccagacttgg agctctgcag
6661 agggtggtgt agggtcttga tttccgtggg cccatgctgc ccagctgcct ccaaggctcc
6721 tggctctgca ggcgactggg ctcctctcct ggtaaactgc tcccaggtcc tggcttgtcc
6781 actagatggg cctgcccccc gggtcttcag tctccccgtt ggtgggcctg gccctggcac
6841 gcctctctgg gcaggtgggc tcccctggac aatgccctgt gccctgtgac ttcacaggtc
6901 cgggcagagc accctggagg ggaggggagg ggacacacgg cccagctctg agaaagcccc
6961 ggggagggga caagatgtgg aggctcctgg gaacctcatc ccgccctctt cctacacagg
7021 acgggaaact gaggctgggg atgggcaggg gcagctctgg gaaggggtt gttcagaggg
7081 gcctctgctc ccactcgggt catggccttc acacgcacct cggcccgcag gggcccctta
7141 ctggacacgg cccgagcgga tggacaagaa gctgctggcc gtgccggccg ccaacaccgt
7201 ccgcttccgc tgcccagccg ctggcaaccc cactccctcc atctcctggc tgaagaacgg
7261 cagggagttc cgcggcgagc accgcattgg aggcatcaag gtgggcgcgg cggggtggct
7321 ctgggcctgg caggcgcggt ggttgctgcc tccgctcact cacccgcccg cgtcccggtg
7381 cagctgcggc atcagcagtg gagcctggtc atggaaagcg tggtgccctc ggaccgcggc
7441 aactacacct gcgtcgtgga gaacaagttt ggcagcatcc ggcagacgta cacgctggac
7501 gtgctgggtg agggccctgg ggcggcgcgg gggtgggggc ggcagtggcg gtggtggtga
7561 gggaggggggt ggcccctgag cgtcatctgc ccccacagag cgctccccgc accggcccat
7621 cctgcaggcg gggctgccgg ccaaccagac ggcggtgctg ggcagcgacg tggagttcca
7681 ctgcaaggtg tacagtgacg cacagcccca catccagtgg ctcaagcacg tggaggtgaa
7741 tggcagcaag gtgggcccgg acggcacacc ctacgttacc gtgctcaagg tgggccaccg
7801 tgtgcacgtg ggtgccgccg ctggggctcc tgggctggcc ccaagggtgc cccttggctg
7861 cgggttgcgt gaggatttgg gtctaggggt tggagcttcg ggggcagaag ctgtgggggt
7921 gcttgtgggg ccaagtctca gccaccccac acctcagggc cataggcagc tgcgttggga
7981 cccgtttccg tgtctgcaga gggccagcct cagccactga agtccctgac atggagctgc
8041 ccacgggctt cttgggggtg ggtgcggctt gggcagcagt ggtgccccag gacaggaggg
8101 cagtgtggcc aagccctcca ggccccctct gggcctcaga ggcggtggct gagccccgac
8161 ctggccgatt ggctctcgtc agctgtgtgc agtggggccc gagctcactg tctgcccgcc
8221 tcctgaagcc cttagctttg ttcccatggc tgccgggtgg gggccactga attgggacgg
8281 ttgcgacact caaagcccaa agagaaacat ctgttcagag agaagacggt ctcttggggg
8341 cggggagcag gcgcagggcg agggtggagt ccagaccccg cccagagagg ccgcctcggg
8401 ccctgtccag ggtacaggtt ctgcaagagc ccgggggagg gcaggccagt gaccagaggt
8461 tgtctgaggg tctgggctgg gttgttgggg tggaggcaga gacgtgcatc ctgtgaaacc
8521 acagccaccg tgaagtgcct ccacgcctcc tccaggcagc ctttggggct gacgcagccc
8581 agcctcgatc tgtaccttgg gggtctccca catcctgcct cgtgcccggc ggggctgcct
8641 cgggggcgtg cctgagccgg gtctcttgtc cccgcagtcc tggatcagtg agagtgtgga
8701 ggccgacgtg cgcctccgcc tggccaatgt gtcggagcgg gacgggggcg agtacctctg
8761 tcgagccacc aatttcatag gcgtggccga gaaggccttt tggctgagcg ttcacgggcc
8821 ccgagcaggt aacgactctg tcccatgccg gccggcacaa gagctccagc tccaaggccc
8881 tggccgcgcg ccctgcacgc cccgcacgcc cagccctgct cgctcccgcc ccggctcgcg
8941 ctccactcgg ggccgcctcg gcaaggctgg cagctccagc ctccacggtg accgcccgct
9001 tcgagccctg tggcctgcgc cgacccttcc cgcacgcctg cgacccccac aggaggtgcc

```
 9061 cggtgcccac cgggccggct ccgtgccgtc tgtgagcacc cctttgcgcc tctctccacc
 9121 cctgcccgct gcctgctcgc ttccgcagcc tgtgtgtccc tgtgtccatc ctccacctgc
 9181 acccgcccgg ctctgcgcta acccgcatgc tgcctgcccg cctgccgctc acctgggaca
 9241 gaggactcgc cggtggaggg gcctggcttc gggctcagta ccggtgtacc aggcggaggg
 9301 ccctcagccg cgtggcggtg accaagttgg cgatggctga ggagttggtg gtggcggcgt
 9361 tttccttgca gcggctggat cctgccgtgt ggactctgtg cggtgcccgc agggcggtgc
 9421 tggcgctcgc ctatcgctct gctctctctt tgtagacggc gggcgctaac accaccgaca
 9481 aggagctaga ggttctctcc ttgcacaacg tcacctttga ggacgccggg gagtacacct
 9541 gcctggcggg caattctatt gggttttctc atcactctgc gtggctggtg gtgctgccag
 9601 gtaccggctt ctgctgctgc tgctgctccg cactgtctgg gggacgctgg ctcgggacac
 9661 gccaaagctg ccaggacgga cgggaatcct gtgacttacg gccgtcccgc ttcttgagcc
 9721 ctcactcctg gccctgtgcc cagtgtgggg acaaagttgg cctggcccgg tcctggtccc
 9781 agaggggccc cctcagcccc ctcgagccca cttcccatct gggtccccaa aggcctctcc
 9841 tgtggctctg gtgtctcccg ggcgcctggt ggcggtgtgg gactggctgg ctctgctggg
 9901 ctccttctct ccagggtctg gccctctaga ctcactggcg ttactgactg cgagaccctc
 9961 cagacaaggc gcgtgctgag gttctgagcc cccttccgct cccagtggtg cctgcggctc
10021 tgggccaggg gcatccatgg gagccccgtg gggggggggg ccaggccagg cctcaacgcc
10081 catgtctttg cagccgagga ggagctggtg gaggctgacg aggcgggcag tgtgtatgca
10141 ggcatcctca gctacggggt gggcttcttc ctgttcatcc tggtggtggc ggctgtgacg
10201 ctctgccgcc tgcgcagccc ccccaagaaa ggcctgggct cccccaccgt gcacaagatc
10261 tcccgcttcc cgctcaagcg acaggtaaca gaaagtagat accaggttct gagctgcctg
10321 cccgccaggc ctcctggagc cccacctcgg cccacgctgg tcctgggctg tgtgagccct
10381 ctctgcagcc aggcgggctc ccctctcctc gtctctgctc accatgtaga gcctagggta
10441 ctttggggca cgaaacattc taaaaatctt cattcaatgc tggtggaagt cagaacgccc
10501 ccccttctgg cccagcactg acccccggct gtacctccac gccctgtcgc ccacgcggcg
10561 ccaacctgcc cctgctgacc caagcaggtg tccctggagt ccaacgcgtc catgagctcc
10621 aacacaccac tggtgcgcat cgcaaggctg tcctcagggg agggccccac gctggccaat
10681 gtctccgagc tcgagctgcc tgccgacccc aaatgggagc tgtctcgggc ccggtcagtg
10741 gtgctgaggg ccagcgttgg ctgtaggggg cttggtggtg ggggtgaaac agccaccagt
10801 cagaggcccg gctgggttta ggggccgtca gggatgtggc ggatgttggg tgtggctggg
10861 gttctgtgga catgctcctg ggacgggtgt atggcaggga ctgcccctct caaggtgccc
10921 tgtctggagg ggcagcaagg gcgggaggct gtgggtgaca ctcttcgtcc ttacgagcag
10981 gctgtagggg gagcatggag ggcttcctgg aggtggtggc tctgggcctc aagggctggg
11041 ccaggctggg gtggggaccg tggtgggctg agagtgggcg agtttgcaca ctcatggtcc
11101 ctctgcctcc actgccaggc tgaccctggg caagcccctt ggggagggct gcttcggcca
11161 ggtggtcatg gcggaggcca tcggcattga caaggaccgg gccgccaagc ctgtcaccgt
11221 agccgtgaag atgctgaaag gtgaggaggg ggcggccagg ggtgcagagc agggctgggg
11281 gcgccgccgc cgcctgacac aggccccccg ctccgtgcac agacgatgcc actgacaagg
11341 acctgtcgga cctggtgtct gagatggaga tgatgaagat gatcgggaaa cacaaaaaca
11401 tcatcaacct gctgggcgcc tgcacgcagg gcggtaggtg cggtagcggc ggtggtgccg
11461 gctgggcggc cctcctgggc ctggcagccc gtctgaggag cccgtgtccc cagggccctt
11521 gtacgtgctg gtggagtacg cggccaaggg taacctgcgg gagtttctgc gggcgcggcg
11581 gcccccgggc ctggactact ccttcgacac ctgcaagccg cccgaggagc agctcacctt
11641 caaggacctg gtgtcctgtg cctaccaggt ggcccggggc atggagtact tggcctccca
11701 gaaggtgggc agggcggcag gtgtgggtgg agtaggctgg gccctgccct gagatgctgg
11761 gagcagcggg gagaggtgga gaggcttcag ccctgcctcc caccccttcc ccagtgcatc
11821 cacagggacc tggctgcccg caatgtgctg gtgaccgagg acaacgtgat gaagatcgca
11881 gacttcgggc tggcccggga cgtgcacaac ctcgactact acaagaagac aaccaacgtg
11941 agcccggccc tggggtgcgg gggtgggggt catgccagta ggacgcctgg cgccaacacc
12001 gccttcccac accctcccag ggccggctgc ccgtgaagtg gatggcgcct gaggccttgt
```

12061 ttgaccgagt ctacactcac cagagtgacg tgtacgtgtc ctgcagagct caggcttcag
12121 gggtggaggc gggaactggg cagagccagg accccagctg cagtccccag gcctgtgccc
12181 tggagctcct gggtgtggtt tctacccctc cctgggggca gcagcgcagc cctggcctat
12241 tcccctggtg cccgcccagg tgtctgtcct gggagtctca ggacagcctg acctcacctt
12301 cccctgcagc tggtcctttg gggtcctgct ctgggagatc ttcacgctgg ggggctcccc
12361 gtaccccggc atccctgtgg aggagctctt caagctgctg aaggagggcc accgcatgga
12421 caagcccgcc aactgcacac acgacctgtg agtggcatcc ctggccctcc actgggtcct
12481 caggggtggg ggtccctccg gggctgggcg ggggagggac tggcagccct tcaggctgtt
12541 cccgaataag gcgggaagcg gcggggctca ctcctgagcg ccctgcccgc aggtacatga
12601 tcatgcggga gtgctggcat gccgcgccct cccagaggcc caccttcaag cagctggtgg
12661 aggacctgga ccgtgtcctt accgtgacgt ccaccgacgt gagtgctggc tctggcctgg
12721 tgccacccgc ctatgcccct ccccctgccg tccccggcca tcctgccccc cagagtgctg
12781 aggtgtgggg cgggccttct ggggcacagc ctgggcacag aggtggctgt gcgaagaggg
12841 gctcggtggc acagcgctca ccccgcctcc cgccagcagg agtacctgga cctgtcggcg
12901 cctttcgagc agtactcccc gggtggccag gacaccccca gctccagctc ctcaggggac
12961 gactccgtgt ttgcccacga cctgctgccc ccggccccac ccagcagtgg gggctcgcgg
13021 acgtgaaggg ccactggtcc ccaacaatgt gaggggtccc tagcagccca ccctgctgct
13081 ggtgcacagc cactccccgg catgagactc agtgcagatg gagagacagc tacacagagc
13141 tttggtctgt gtgtgtgtgt gtgcgtgtgt gtgtgtgtgt gcacatccgc gtgtgcctgt
13201 gtgcgtgcgc atcttgcctc caggtgcaga ggtaccctgg gtgtccccgc tgctgtgcaa
13261 cggtctcctg actggtgctg cagcaccgag gggcctttgt tctgggggga cccagtgcag
13321 aatgtaagtg ggcccacccg gtgggacccc gtggggcagg gagctgggcc cgacatggct
13381 ccggcctctg cctttgcacc acgggacatc acagggtggg cctcggcccc tcccacaccc
13441 aaagctgagc ctgcagggaa gccccacatg tccagcacct tgtgcctggg gtgttagtgg
13501 caccgcctcc ccacctccag gctttcccac ttcccaccct gcccctcaga gactgaaatt
13561 acgggtacct gaagatggga gcctttacct tttatgcaaa aggtttattc cggaaactag
13621 tgtacatttc tataaataga tgctgtgtat atggtatata tacatatata tatataacat
13681 atatggaaga ggaaaaggct ggtacaacgg aggcctgcga ccctgggggc acaggaggca
13741 ggcatggccc tgggcggggc gtgggggggc gtggagggag gccccagggg gtctcaccca
13801 tgcaagcaga ggaccagggc tttttctggc accgcagttt tgttttaaaa ctggacctgt
13861 atatttgtaa agctatttat gggcccctgg cactcttgtt cccacacccc aacacttcca
13921 gcatttagct ggccacatgg cggagagttt taatttttaa cttattgaca accgagaagg
13981 tttatcccgc cgatagaggg acggccaaga atgtacgtcc agcctgcccc ggagctggag
14041 gatcccctcc aagcctaaaa ggttgttaat agttggaggt gattccagtg aagatatttt
14101 atttcctttg tccttttttca ggagaattag atttctatag gatttttctt taggagattt
14161 atttttttgga cttcaaagca agctggtatt ttcatacaaa ttcttctaat tgctgtgtgt
14221 cccaggcagg gagacggttt ccagggaggg gccggccctg tgtgcaggtt ccgatgttat
14281 tagatgttac aagtttatat atatctatat atataattta ttgagttttt acaagatgta
14341 tttgttgtag acttaacact tcttacgcaa tgcttctaga gttttatagc ctggactgct
14401 acctttcaaa gcttggaggg aagccgtgaa ttcagttggt tcgttctgta ctgttactgg
14461 gccctgagtc tgggcagctg tcccttgctt gcctgcaggg ccatggctca gggtggtctc
14521 ttcttggggc ccagtgcatg gtggccagag gtgtcaccca aaccggcagg tgcgattttg
14581 ttaacccagc gacgaacttt ccgaaaaata aagacacctg gttgctaacc tggccctgtg
14641 ctttctgtct ccagttctgg gataggggag ggaggggtca ctttgccagg tggtcccagt
14701 tgcgcgggat ggatgctggc agcagcaccg aaagtcactg gtgggctggg agccccaaga
14761 gcaaggaatg tttatgggag gggcctggcg gaagggagca gggtgcctgg gggtgcactg
14821 ccctggctgc tcccagcttg tgggttcctg aggtggtggt ggtggtgggg agggtccttt
14881 ctcactagct ctgaggcaga ccttctctca tcaccccact cctggcatcc gccttcccag
14941 tcagctgggg agctttctgg gcatccctct atggagccaa aagcaagcaa agccctcatg
15001 gggccctggg ggctacacag gcggtcactc tcctccagat cagctctctg ccctcccagg

```
15061 ccgggcaacc agtgccccca ctgccttggg ctccatcagg gtcccctaca gtgataaagc
15121 acctttgggc agatgaggtg ctgagaaccc agagatggaa ccaggccctt gcccaagttc
15181 atagccctag cagggtggga ggacaacatg gtgagagcaa gtctgggaag gcttcctgga
15241 ggaggtgtgc cgtctctcct gactccccac caccctcttt gctgtcctcc cttctgctat
15301 cctccctctc ttgtcctccc gtttttccca tctctgctgt ccccacctct gtcgtcctcc
15361 ttctgctctc ctccccccat cccctctgct ctccctacct ctgctgtccc ctctgccgtc
15421 ctccctctgc tctcctcccc tctgctggct caagagcagg gtttcccaac catgagctgc
15481 atgaactcta gcttctaaaa tgctctggct acaaactcac ctttcaggtc agggggtact
15541 gctggcccgt ttcctgggca ggcaagggtt taactcaacc ccattcaggg aagcacgtgt
15601 gggcgcaggc ctggtggaag tggccttaca agggactctg catccctaat gcccccactt
15661 gcccagaaac cctatgctgg gccccagagg caggcctggc catgggacgc ctggtgacag
15721 tggcaggatg gggaggccca catgggcctg aaggctgagg cctgcagggc agtgggggga
15781 ccaggccaac aggcaggcag tgccagcatc cacaccaagg caggcagagc atggggctcg
15841 aagcgcgggc cgggagcgcc ccctagcgct ggctgggcag tgtccctgct acaaacccaa
15901 ggcccctctc ctgtcagggc tctggtggac ctctggtggg cacagtggga tcctgaatgg
15961 gtgctgggga ccaaagggct gggccaccgg gagaacagtg gcccatgaag gtgctggtgg
16021 gccagccccc tcctcctcag cgtgcttcct tagcgacccc agatggcagg gcacagtccc
16081 tgaagctgcc ccaccagggg ctccctggct gcctccccgt cccataaggt gagcccatga
16141 gagaccccag ctgtcagcac aactgaacct ccgccatcag ggtgccctct agtggttggg
16201 tgtgctctag gctggcaggg tccccgccct tgctgtctgc tgatggctga gggggacatg
16261 tctcatggga ggcccagctt ccaggacaca actggtggct cctggggtca ccaagggcac
16321 ctggtttgtt cacagctctt tgggctgctg tccccatgag ggagcacctc ccaccccagc
16381 tgtgggtcca tcatttcctc tgattaatta gggcctaggg gtcaagggag gccccgaggg
16441 aggactctca gtgtgaacaa accagcagcc agggccgcag agaagcctgt gaggtgccca
16501 cagggcctgg tcccagtgtg ggcagagcac ctaagggatg gcttctgtcc actgagaagg
16561 gtcgggagcc aagacaccac actgctatcc tggcgctgga accatccacg cactcctgca
16621 gccaggccac gctgaggcag gtaggcaccc agaggtccgg gctgggggct gctctccatg
16681 gccccaggcc atcacacatc cctcagggcg tctgggccct gcctgtgggc tggactgcag
16741 gctgaaggcc ctgcctcatc caggactccc tagggcagta ctcggtgctc tttcccctca
16801 gcggcctgag gagtctttca gaagagctgg ccctcctggg tgacacctcg gcgagggtcc
16861 cagcccctaa ccccaggact cccaagaagt cactgaggtc cccagagcag ggagagcatg
16921 accaggtggc agggccactg gcctggagaa cgtcccacac tgttccatga gcagct
```

//

F245114. Homo sapiens fibr...[gi:7533124]

Links

```
LOCUS       AF245114                2184 bp    mRNA    linear   PRI 28-MAR-2002
DEFINITION  Homo sapiens fibroblast growth factor receptor 3 (FGFR3) mRNA,
            complete cds, alternatively spliced.
ACCESSION   AF245114
VERSION     AF245114.1  GI:7533124
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2184)
  AUTHORS   Terada,M., Shimizu,A., Sato,N., Miyakaze,S.I., Katayama,H. and
            Kurokawa-Seo,M.
  TITLE     Fibroblast growth factor receptor 3 lacking the Ig IIIb and
            transmembrane domains secreted from human squamous cell carcinoma
            DJM-1 binds to FGFs
  JOURNAL   Mol. Cell Biol. Res. Commun. 4 (6), 365-373 (2001)
  MEDLINE   21561228
   PUBMED   11703096
REFERENCE   2  (bases 1 to 2184)
  AUTHORS   Terada,M., Shimizu,A. and Seo,M.
  TITLE     Secretion and dimerization of the FGFR3 isoform, resulting from
            alternative splicing, that is expressed in human malignant
            trichilemmal cyst cell
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 2184)
  AUTHORS   Terada,M., Shimizu,A. and Seo,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-MAR-2000) Biotechnology, Kyoto Sangyo University,
            Kamigamo-Motoyama, Kita-Ku, Kyoto 603-8555, Japan
FEATURES             Location/Qualifiers
     source          1..2184
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="4"
                     /map="4p16.3"
                     /cell_line="DJM-1"
                     /cell_type="malignant trichilemmal cyst cell"
     gene            1..2184
                     /gene="FGFR3"
     CDS             40..2124
                     /gene="FGFR3"
                     /note="tyrosine kinase; IgIII C-terminal and transmembrane
                     deleted isoform; alternatively spliced"
                     /codon_start=1
```

/product="fibroblast growth factor receptor 3"
/protein_id="AAF63380.1"
/db_xref="GI:7533125"
/translation="MGAPACALALCVAVAIVAGASSESLGTEQRVVGRAAEVPGPEPG
QQEQLVFGSGDAVELSCPPPGGGPMGPTVWVKDGTGLVPSERVLVGPQRLQVLNASHE
DSGAYSCRQRLTQRVLCHFSVRVTDAPSSGDDEDGEDEAEDTGVDTGAPYWTRPERMD
KKLLAVPAANTVRFRCPAAGNPTPSISWLKNGREFRGEHRIGGIKLRHQQWSLVMESV
VPSDRGNYTCVVENKFGSIRQTYTLDVLERSPHRPILQAGLPANQTAVLGSDVEFHCK
VYSDAQPHIQWLKHVEVNGSKVGPDGTPYVTVLKVSLESNASMSSNTPLVRIARLSSG
EGPTLANVSELELPADPKWELSRARLTLGKPLGEGCFGQVVMAEAIGIDKDRAAKPVT
VAVKMLKDDATDKDLSDLVSEMEMMKMIGKHKNIINLLGACTQGGPLYVLVEYAAKGN
LREFLRARRPPGLDYSFDTCKPPEEQLTFKDLVSCAYQVARGMEYLASQKCIHRDLAA
RNVLVTEDNVMKIADFGLARDVHNLDYYKKTTNGRLPVKWMAPEALFDRVYTHQSDVW
SFGVLLWEIFTLGGSPYPGIPVEELFKLLKEGHRMDKPANCTHDLYMIMRECWHAAPS
QRPTFKQLVEDLDRVLTVTSTDEYLDLSAPFEQYSPGGQDTPSSSSSGDDSVFAHDLL
PPAPPSSGGSRT"

BASE COUNT 386 a 722 c 732 g 344 t

ORIGIN

```
      1 cgcgcgctgc ctgaggacgc cgcggccccc gcccccgcca tgggcgcccc tgcctgcgcc
     61 ctcgcgctct gcgtggccgt ggccatcgtg gccggcgcct cctcggagtc cttggggacg
    121 gagcagcgcg tcgtggggcg agcggcagaa gtcccgggcc cagagcccgg ccagcaggag
    181 cagttggtct tcggcagcgg ggatgctgtg gagctgagct gtcccccgcc cgggggtggt
    241 cccatggggc ccactgtctg ggtcaaggat ggcacagggc tggtgccctc ggagcgtgtc
    301 ctggtggggc cccagcggct gcaggtgctg aatgcctccc acgaggactc cggggcctac
    361 agctgccggc agcggctcac gcagcgcgta ctgtgccact tcagtgtgcg ggtgacagac
    421 gctccatcct cgggagatga cgaagacggg gaggacgagg ctgaggacac aggtgtggac
    481 acaggggccc cttactggac acggcccgag cggatggaca agaagctgct ggccgtgccg
    541 gccgccaaca ccgtccgctt ccgctgccca gccgctggca accccactcc ctccatctcc
    601 tggctgaaga acggcaggga gttccgcggc gagcaccgca ttggaggcat caagctgcgg
    661 catcagcagt ggagcctggt catggaaagc gtggtgccct cggaccgcgg caactacacc
    721 tgcgtcgtgg agaacaagtt tggcagcatc cggcagacgt acacgctgga cgtgctggag
    781 cgctccccgc accggcccat cctgcaggcg gggctgccgg ccaaccagac ggcggtgctg
    841 ggcagcgacg tggagttcca ctgcaaggtg tacagtgacg cacagcccca catccagtgg
    901 ctcaagcacg tggaggtgaa cggcagcaag gtgggcccgg acggcacacc ctacgttacc
    961 gtgctcaagg tgtccctgga gtccaacgcg tccatgagct ccaacacacc actggtgcgc
   1021 atcgcaaggc tgtcctcagg ggagggcccc acgctggcca atgtctccga gctcgagctg
   1081 cctgccgacc ccaaatggga gctgtctcgg gcccggctga ccctgggcaa gccccttggg
   1141 gagggctgct tcggccaggt ggtcatggcg gaggccatcg gcattgacaa ggaccgggcc
   1201 gccaagcctg tcaccgtagc cgtgaagatg ctgaaagacg atgccactga caaggacctg
   1261 tcggacctgg tgtctgagat ggagatgatg aagatgatcg ggaaacacaa aaacatcatc
   1321 aacctgctgg gcgcctgcac gcagggcggg cccctgtacg tgctggtgga gtacgcggcc
   1381 aagggtaacc tgcgggagtt tctgcgggcg cggcggcccc cgggcctgga ctactccttc
   1441 gacacctgca agccgcccga ggagcagctc accttcaagg acctggtgtc ctgtgcctac
   1501 caggtggccc ggggcatgga gtacttggcc tcccagaagt gcatccacag ggacctggct
   1561 gcccgcaatg tgctggtgac cgaggacaac gtgatgaaga tcgcagactt cgggctggcc
   1621 cgggacgtgc acaacctcga ctactacaag aagacaacca acggccggct gcccgtgaag
   1681 tggatggcgc ctgaggcctt gtttgaccga gtctacactc accagagtga cgtctggtcc
   1741 tttggggtcc tgctctggga gatcttcacg ctgggggget ccccgtaccc cggcatccct
   1801 gtggaggagc tcttcaagct gctgaaggag ggccaccgca tggacaagcc cgccaactgc
   1861 acacacgacc tgtacatgat catgcgggag tgctggcatg ccgcgccctc ccagaggccc
```

```
1921 accttcaagc agctggtgga ggacctggac cgtgtcctta ccgtgacgtc caccgacgag
1981 tacctggacc tgtcggcgcc tttcgagcag tactccccgg gtggccagga cacccccagc
2041 tccagctcct caggggacga ctccgtgttt gcccacgacc tgctgccccc ggccccaccc
2101 agcagtgggg gctcgcggac gtgaagggcc actggtcccc aacaatgtga ggggtcccta
2161 gcagccctcc ctgctgctgg tgca
```

>gi|7533124|gb|AF245114.1| Homo sapiens fibroblast growth factor receptor 3 (FGFR3) mRNA,
complete cds, alternatively spliced
Length = 2184

Score = 2397 bits (1209), Expect = 0.0
Identities = 1215/1217 (99%)
Strand = Plus / Plus

```
Query: 1040 aggtgtccctggagtccaacgcgtccatgagctccaacacaccactggtgcgcatcgcaa 1099
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 968  aggtgtccctggagtccaacgcgtccatgagctccaacacaccactggtgcgcatcgcaa 1027

Query: 1100 ggctgtcctcaggggagggccccacgctggccaatgtctccgagctcgagctgcctgccg 1159
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1028 ggctgtcctcaggggagggccccacgctggccaatgtctccgagctcgagctgcctgccg 1087

Query: 1160 accccaaatgggagctgtctcgggcccggctgaccctgggcaagccccttggggagggct 1219
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1088 accccaaatgggagctgtctcgggcccggctgaccctgggcaagccccttggggagggct 1147

Query: 1220 gcttcggccaggtggtcatggcggaggccatcggcattgacaaggaccgggccgccaagc 1279
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1148 gcttcggccaggtggtcatggcggaggccatcggcattgacaaggaccgggccgccaagc 1207

Query: 1280 ctgtcaccgtagccgtgaagatgctgaaagacgatgccactgacaaggacctgtcggacc 1339
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1208 ctgtcaccgtagccgtgaagatgctgaaagacgatgccactgacaaggacctgtcggacc 1267

Query: 1340 tggtgtctgagatggagatgatgaagatgatcgggaaacacaaaaacatcatcaacctgc 1399
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1268 tggtgtctgagatggagatgatgaagatgatcgggaaacacaaaaacatcatcaacctgc 1327

Query: 1400 tgggcgcctgcacgcagggcgggcccctgtacgtgctggtggagtacgcggccaagggta 1459
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1328 tgggcgcctgcacgcagggcgggcccctgtacgtgctggtggagtacgcggccaagggta 1387

Query: 1460 acctgcgggagtttctgcgggcgcggcggcccccgggcctggactactccttcgacacct 1519
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1388 acctgcgggagtttctgcgggcgcggcggcccccgggcctggactactccttcgacacct 1447
```

```
Query: 1520 gcaagccgcccgaggagcagctcaccttcaaggacctggtgtcctgtgcctaccaggtgg 1579
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1448 gcaagccgcccgaggagcagctcaccttcaaggacctggtgtcctgtgcctaccaggtgg 1507


Query: 1580 cccggggcatggagtacttggcctcccagaagtgcatccacagggacctggctgcccgca 1639
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1508 cccggggcatggagtacttggcctcccagaagtgcatccacagggacctggctgcccgca 1567


Query: 1640 atgtgctggtgaccgaggacaacgtgatgaagatcgcagacttcgggctggcccgggacg 1699
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1568 atgtgctggtgaccgaggacaacgtgatgaagatcgcagacttcgggctggcccgggacg 1627


Query: 1700 tgcacaacctcgactactacaagaagacaaccaacggccggctccccgtgaagtggatgg 1759
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct: 1628 tgcacaacctcgactactacaagaagacaaccaacggccggctgcccgtgaagtggatgg 1687


Query: 1760 cgcctgaggccttgtttgaccgagtctacactcaccagagtgacgtctggtcctttgggg 1819
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1688 cgcctgaggccttgtttgaccgagtctacactcaccagagtgacgtctggtcctttgggg 1747


Query: 1820 tcctgctctgggagatcttcacgctgggggctccccgtaccccggcatccctgtggagg 1879
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1748 tcctgctctgggagatcttcacgctgggggctccccgtaccccggcatccctgtggagg 1807


Query: 1880 agctcttcaagctgctgaaggagggccaccgcatggacaagcccgccaactgcacacacg 1939
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1808 agctcttcaagctgctgaaggagggccaccgcatggacaagcccgccaactgcacacacg 1867


Query: 1940 acctgtacatgatcatgcgggagtgctggcatgccgcgccctcccagaggcccaccttca 1999
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1868 acctgtacatgatcatgcgggagtgctggcatgccgcgccctcccagaggcccaccttca 1927


Query: 2000 agcagctggtggaggacctggaccgtgtccttaccgtgacgtccaccgacgagtacctgg 2059
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1928 agcagctggtggaggacctggaccgtgtccttaccgtgacgtccaccgacgagtacctgg 1987


Query: 2060 acctgtcggcgcctttcgagcagtactccccgggtggccaggacacccccagctccagct 2119
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1988 acctgtcggcgcctttcgagcagtactccccgggtggccaggacacccccagctccagct 2047
```

```
Query: 2120 cctcaggggacgactccgtgtttgcccacgacctgctgcccccggccccacccagcagtg 2179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2048 cctcaggggacgactccgtgtttgcccacgacctgctgcccccggccccacccagcagtg 2107


Query: 2180 ggggctcgcggacgtgaagggccactggtccccaacaatgtgaggggtccctagcagccc 2239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 2108 ggggctcgcggacgtgaagggccactggtccccaacaatgtgaggggtccctagcagccc 2167


Query: 2240 accctgctgctggtgca 2256
             |||||||||||||||
Sbjct: 2168 tccctgctgctggtgca 2184
```

>gi|20452379|gb|AF487554.1| Homo sapiens fibroblast growth factor receptor 3 (FGFR3) gene, partial
cds, alternatively spliced
Length = 16976

Score = 1146 bits (578), Expect = 0.0
Identities = 602/611 (98%), Gaps = 1/611 (0%)
Strand = Plus / Plus

```
Query: 2853  ggaagaggaaaaggctggtacaacggaggcctgcgaccctgggggcacaggaggcaggca 2912
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13685 ggaagaggaaaaggctggtacaacggaggcctgcgaccctgggggcacaggaggcaggca 13744


Query: 2913  tggccctgggcggggcgtnnnnnnncgtggagggaggccccagggg-tctcacccatgca 2971
              |||||||||||||||||       ||||||||||||||||||| ||||||||||||
Sbjct: 13745 tggccctgggcggggcgtgggggggcgtggagggaggccccaggggtctcacccatgca 13804


Query: 2972  agcagaggaccagggctttttctggcaccgcagttttgttttaaaactggacctgtatat 3031
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13805 agcagaggaccagggctttttctggcaccgcagttttgttttaaaactggacctgtatat 13864


Query: 3032  ttgtaaagctatttatgggcccctggcactcttgttcccacaccccaacacttccagcat 3091
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13865 ttgtaaagctatttatgggcccctggcactcttgttcccacaccccaacacttccagcat 13924


Query: 3092  ttagctggccacatggcggagagttttaatttttaacttattgacaaccgagaaggttta 3151
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13925 ttagctggccacatggcggagagttttaatttttaacttattgacaaccgagaaggttta 13984


Query: 3152  tcccgccgatagagggacggccaagaatgtacgtccagcctgccccggagctggaggatc 3211
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 13985 tcccgccgatagagggacggccaagaatgtacgtccagcctgccccggagctggaggatc 14044


Query: 3212  ccctccaagcctaaaaggttgttaatagttggaggtgattccagtgaagatattttattt 3271
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14045 ccctccaagcctaaaaggttgttaatagttggaggtgattccagtgaagatattttattt 14104


Query: 3272  gctttgtccttttttcaggagaattagatttctataggatttttctttaggagatttattt 3331
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14105 cctttgtccttttttcaggagaattagatttctataggatttttctttaggagatttattt 14164
```

```
Query: 3332  tttggacttcaaagcaagctggtattttcatacaaattcttctaattgctgtgtgtccca 3391
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14165 tttggacttcaaagcaagctggtattttcatacaaattcttctaattgctgtgtgtccca 14224


Query: 3392  ggcagggagacggtttccagggaggggccggccctgtgtgcaggttccgatgttattaga 3451
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 14225 ggcagggagacggtttccagggaggggccggccctgtgtgcaggttccgatgttattaga 14284


Query: 3452  tgttacaagtt 3462
             ||||||||||
Sbjct: 14285 tgttacaagtt 14295
```

FILE 'MEDLINE, BIOSIS, CANCERLIT, LIFESCI, BIOTECHDS, CAPLUS' ENTERED AT 20:01:05 ON 18 JAN 2003

L1 8 S M64347###
L2 7 DUP REM L1 (1 DUPLICATE REMOVED)
L3 7949 S (FGF(W)R) OR (FGF(W)R3) OR (FIBROBLAST(W)GROWTH(W)FACTOR(W)(R
L4 115579 S NEUROCYTOMA# OR PINEALOMA# OR GLIOMA# OR MEDULLOBLASTOMA# OR
L5 132127 S (CEREBRAL OR (CHOROID(W)PLEXUS) OR CEREBELLUM OR HYPOTHALAMIC
L6 10081 S (CEREBRAL OR (CHOROID(W)PLEXUS) OR CEREBELLUM OR HYPOTHALAMIC
L7 204265 S L4 OR L5 OR L6
L8 151 S L3 AND L7
L9 115 S L8 AND PY<2001
L10 136 S L8 AND PY<2002
L11 67 DUP REM L10 (69 DUPLICATES REMOVED)
L12 1822 S (FGFR3 OR (FGF(W)R3) OR (FGF(W)RECEPTOR(W)3) OR (FIBROBLAST(W
L13 15 S L12 AND L7
L14 6 DUP REM L13 (9 DUPLICATES REMOVED)
L15 31656 S GOLUB?/AU OR LANDER?/AU OR POMEROY?/AU OR TAMAYO?/AU
L16 0 S L15 AND L8
L17 1 S L15 AND L12
L18 10 S L15 AND L3
L19 10 S L17 OR L18
L20 4 DUP REM L19 (6 DUPLICATES REMOVED)

10/066,305

L2 ANSWER 5 OF 7 MEDLINE
ACCESSION NUMBER: 2000408205 MEDLINE
DOCUMENT NUMBER: 20349276 PubMed ID: 10889045
TITLE: Repeat polymorphisms within gene regions: phenotypic and evolutionary implications.
AUTHOR: Wren J D; Forgacs E; Fondon J W 3rd; Pertsemlidis A; Cheng S Y; Gallardo T; Williams R S; Shohet R V; Minna J D; Garner H R
CORPORATE SOURCE: Program in Genetics, Southwestern Graduate School of Biomedical Sciences, Dallas, TX, USA.
CONTRACT NUMBER: P50CA70907 (NCI)
SOURCE: AMERICAN JOURNAL OF HUMAN GENETICS, (2000 Aug) 67 (2) 345-56.
Journal code: 0370475. ISSN: 0002-9297.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF013956; GENBANK-AF017789; GENBANK-AF032886; GENBANK-AF042838; GENBANK-AF047437; GENBANK-AF060231; GENBANK-D14838; GENBANK-D83492; GENBANK-D86407; GENBANK-D86550; GENBANK-L08835; GENBANK-M55047; GENBANK-M60052; GENBANK-M60315; GENBANK-**M64347**; GENBANK-R12160; GENBANK-R42196; GENBANK-T47177; GENBANK-T62484; GENBANK-T63962; GENBANK-T70173; GENBANK-U49020; GENBANK-U60325; GENBANK-X55313; GENBANK-X70811; GENBANK-X78261; GENBANK-X82209; GENBANK-Y00285; GENBANK-Y11525; +
ENTRY MONTH: 200008
ENTRY DATE: Entered STN: 20000901
Last Updated on STN: 20030105
Entered Medline: 20000821

AB We have developed an algorithm that predicted 11,265 potentially polymorphic tandem repeats within transcribed sequences. We estimate that 22% (2,207/9,717) of the annotated clusters within UniGene contain at least one potentially polymorphic locus. Our predictions were tested by allelotyping a panel of approximately 30 individuals for 5% of these regions, confirming polymorphism for more than half the loci tested. Our study indicates that tandem-repeat polymorphisms in genes are more common than is generally believed. Approximately 8% of these loci are within coding sequences and, if polymorphic, would result in frameshifts. Our catalogue of putative polymorphic repeats within transcribed sequences comprises a large set of potentially phenotypic or disease-causing loci. In addition, from the anomalous character of the repetitive sequences within unannotated clusters, we also conclude that the UniGene cluster count substantially overestimates the number of genes in the human genome.

We hypothesize that polymorphisms in repeated sequences occur with some baseline distribution, on the basis of repeat homogeneity, size, and sequence composition, and that deviations from that distribution are indicative of the nature of selection pressure at that locus. We find evidence of selective maintenance of the ability of some genes to respond very rapidly, perhaps even on intragenerational timescales, to fluctuating selective pressures.

L2 ANSWER 4 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:758742 CAPLUS
DOCUMENT NUMBER: 135:314390
TITLE: Large-scale monitoring of expression patterns of p53-regulated gene and analysis of p53 gene function
INVENTOR(S): Mack, David H.
PATENT ASSIGNEE(S): Affymetrix, Inc., USA
SOURCE: U.S., 46 pp., Cont.-in-part of Appl. No. PCT/US98/01206.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6303301	B1	20011016	US 1998-86285	19980529
WO 9830722	A1	19980716	WO 1998-US1206	19980112

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG

US 2002028454	A1	20020307	US 2001-836278	20010418

PRIORITY APPLN. INFO.:

US 1997-35327P	P	19970113
WO 1998-US1206	A2	19980112
US 1997-49627P	P	19970613
US 1998-86285	A3	19980529

AB This invention provides methods, compns. and app. for mapping the regulatory relationships of genes by massive parallel monitoring of gene expression. The information obtained can be of use in drug discovery (no data). The method uses high d. oligonucleotide arrays to monitor changes in expression in response to events and stimuli. Very large nos. of gene (>6,500) may be monitored in this method using samples from many tissues and developmental or disease stages. Changes are quantified and a relationship model constructed using LISREL (Linear Structure Relationship) methods. Mutations in up-stream regulatory genes can be detected by monitoring the change in down-stream gene expression. Similarly, the effect of a specific mutation in an up-stream gene is detd. by monitoring the down-stream gene expression. In addn., regulatory function of a target gene can be detd. by monitoring the expression of a large no. of down-stream genes. The invention also provides specific embodiments for detecting p53 functional homozygous and heterozygous mutations and for detg. the function of p53 mutations.

REFERENCE COUNT: 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 1 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:241013 CAPLUS
DOCUMENT NUMBER: 136:277466
TITLE: Expressed gene sets as markers for specific tumors
INVENTOR(S): Ramaswamy, Sridhar; Golub, Todd B.; Tamayo, Pablo; Angelo, Michael
PATENT ASSIGNEE(S): Whitehead Institute for Biomedical Research, USA; Dana-Farber Cancer Institute, Inc.
SOURCE: PCT Int. Appl., 715 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002024956	A2	20020328	WO 2001-US29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002024956	A2	20020328	WO 2001-XA29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002024956	A2	20020328	WO 2001-XB29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
WO 2002024956	A2	20020328	WO 2001-XC29287	20010919
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PH, PL, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

AU 2001092802	A5	20020402	AU 2001-92802		20010919
US 2002110820	A1	20020815	US 2001-955920		20010919
PRIORITY APPLN. INFO.:			US 2000-233534P	P	20000919
			US 2001-278749P	P	20010326
			WO 2001-US29287	W	20010919

AB Sets of genetic markers for specific tumor classes are described, as well as methods of identifying a biol. sample based on these markers. Total RNA was isolated from .apprx.300 human tumor and normal tissue specimens representing 30 individual classes of tumor or normal tissue, and cDNA produced using established mol. biol. protocols was hybridized to two high d. Affymetrix oligonucleotide microarrays (Hu6800FL and Hu35KsubA0). Raw expression data was combined into a master data set contg. the expression values for between 6800 and 16,000 genes expressed by each individual sample. A filter was applied to this data set which only allows those genes expressed at 3-fold above baseline and with an abs. difference in expression value of 100 to pass. By comparing the sets of genes which are expressed specifically in one class of tumor (e.g., pancreatic adenocarcinoma) vs. its accompanying normal tissue (e.g., normal pancreas), sets of genes were detd. which are specific to various tumors and their normal tissue counterparts. Also described are diagnostic, prognostic, and therapeutic screening uses for these markers, as well as oligonucleotide arrays comprising these markers. [This abstr. record is one of 4 records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

L2 ANSWER 2 OF 7 CAPLUS COPYRIGHT 2003 ACS

L2 ANSWER 7 OF 7 MEDLINE DUPLICATE 1

ACCESSION NUMBER: 92147110 MEDLINE
DOCUMENT NUMBER: 92147110 PubMed ID: 1664411
TITLE: A gene encoding a fibroblast growth factor receptor isolated from the Huntington disease gene region of human chromosome 4.
AUTHOR: Thompson L M; Plummer S; Schalling M; Altherr M R; Gusella J F; Housman D E; Wasmuth J J
CORPORATE SOURCE: Department of Biological Chemistry, College of Medicine, University of California, Irvine 92717.
CONTRACT NUMBER: NS25631-04 (NINDS)
SOURCE: GENOMICS, (1991 Dec) 11 (4) 1133-42.
Journal code: 8800135. ISSN: 0888-7543.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-**M64347**
ENTRY MONTH: 199203
ENTRY DATE: Entered STN: 19920405
Last Updated on STN: 20000303
Entered Medline: 19920313

AB The gene responsible for Huntington disease (HD), an autosomal dominant neurodegenerative disorder, is located near the terminus of the short arm of chromosome 4. Detailed genetic linkage and physical mapping studies have defined a region of approximately 2.5 million basepairs where the disease gene is likely to be located. Efforts to identify the disease gene are now focused on the identification and characterization of expressed genes in this region. Nucleotide sequence analysis of a cDNA clone derived from the HD gene region has revealed that it encodes a member of the fibroblast growth factor subfamily of tyrosine kinase receptors, some members of which are known to be involved in the differentiation and survival of certain cell types within the central nervous system. Histochemical analysis using in situ hybridization revealed its expression in many areas of the brain, among them being the caudate and putamen. The nature of this gene, FGFR3, and its map location make it a possible candidate for the HD gene.

L2 ANSWER 6 OF 7 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:641026 CAPLUS
DOCUMENT NUMBER: 131:267987
TITLE: Cancer diagnosis and therapy based on expression levels of p53-regulated genes
INVENTOR(S): Levine, Arnold J.; Murphy, Maureen E.; Mack, David H.; Gish, Kurt C.; Tom, Edward Yat Wah
PATENT ASSIGNEE(S): Affymetrix, Inc., USA; Princeton University
SOURCE: PCT Int. Appl., 46 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9950456	A1	19991007	WO 1999-US6656	19990326
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6020135	A	20000201	US 1998-49025	19980327
CA 2324444	AA	19991007	CA 1999-2324444	19990326
AU 9932085	A1	19991018	AU 1999-32085	19990326
EP 1064404	A1	20010103	EP 1999-914184	19990326
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
US 6171798	B1	20010109	US 1999-442039	19991117
US 2001039013	A1	20011108	US 2001-755028	20010108

PRIORITY APPLN. INFO.:
US 1998-49025 A1 19980327
WO 1999-US6656 W 19990326
US 1999-442039 A3 19991117

AB Many genes are identified as being p53-regulated which were not heretofore known to be p53-regulated. This includes both genes whose expression is induced and genes whose expression is repressed by the expression of wild-type p53. The effects of p53 expression on gene expression in Eb-1 cells was tested by hybridizing to a chip that contains deoxyoligonucleotide sequences (25-mers) that derived from a database of 6800 known genes or EST sequences. Seventy genes were induced by p53 and 77 were repressed by p53. Monitoring expression of these genes is used to provide indications of p53 status in a cell. Such monitoring can also be used to screen for useful anticancer therapeutics, as well as for substances which are carcinogenic. Defects in p53 can be bypassed by supplying p53 induced genes to cells. Defects in p53 can also be bypassed by supplying antisense constructs to p53-repressed genes.

REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 66 OF 67 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:79455 CAPLUS
DOCUMENT NUMBER: 114:79455
TITLE: Suppression of basic fibroblast growth factor expression by antisense oligodeoxynucleotides inhibits the growth of transformed human astrocytes
AUTHOR(S): Morrison, Richard S.
CORPORATE SOURCE: Robert S. Dow Neurol. Sci. Inst., Good Samaritan Hosp., Portland, OR, 97209, USA
SOURCE: Journal of Biological Chemistry (**1991**), 266(2), 728-34
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Basic fibroblast growth factor (bFGF) is a heparin-binding protein expressing potent mitogenic and angiogenic properties. Elevated levels of bFGF have recently been described in human **glioma** cell lines. The high degree of vascularity and invasiveness which characterize human **gliomas** suggest that activated expression of bFGF or similar proteins may be related to the aberrant growth patterns of these tumors. The influence of endogenous bFGF on **glioma** cell growth in vitro was evaluated in the present study by downregulating bFGF expression using antisense oligonucleotide primers. The addn. of 50 .mu.M bFGF-specific antisense primer to the human **glioma** cell line SNB-19 resulted in an 80% inhibition in **glioma** growth. This effect was saturable and specific. Antisense primers directed to 2 different sites of bFGF mRNA were effective in suppressing SNB-19 growth, whereas sense strand primer was ineffective. Furthermore, only the antisense primer significantly reduced the specific activity of bFGF protein in SNB-19 cell exts. Neither antisense or sense primers inhibited the growth of non-transformed human glia. BFGF mRNA was detected in both transformed and nontransformed human glia by polymerase chain reaction anal. suggesting that alterations in bFGF isoform content or activity may be specifically related to abnormal growth control in human **gliomas**.

L11 ANSWER 65 OF 67 MEDLINE DUPLICATE 26

ACCESSION NUMBER: 91342665 MEDLINE
DOCUMENT NUMBER: 91342665 PubMed ID: 1652059
TITLE: The human **fibroblast growth factor receptor** genes: a common structural arrangement underlies the mechanisms for generating receptor forms that differ in their third immunoglobulin domain.
AUTHOR: Johnson D E; Lu J; Chen H; Werner S; Williams L T
CORPORATE SOURCE: Howard Hughes Medical Institute, Program of Excellence in Molecular Biology, University of California, San Francisco 94143-0724.
CONTRACT NUMBER: HL-43821 (NHLBI)
SOURCE: MOLECULAR AND CELLULAR BIOLOGY, **(1991 Sep)** 11 (9) 4627-34.
Journal code: 8109087. ISSN: 0270-7306.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199109
ENTRY DATE: Entered STN: 19911013
Last Updated on STN: 19970203
Entered Medline: 19910920

AB To determine the mechanisms by which multiple forms of fibroblast growth factor (FGF) receptors are generated, we have mapped the arrangement of exons and introns in the human FGF receptor 1 (FGFR 1) gene (flg). We found three alternative exons encoding a portion of the third immunoglobulin (Ig)-like domain of the receptor. One of these alternatives encodes a sequence that is part of a secreted form of FGFR 1. The other two encode sequences that are likely part of transmembrane forms of FGFR 1. One of these forms has not been previously reported in published cDNAs.

Also, we have determined the structural organization of a portion of the human FGFR 2 gene (bek) and found a similar arrangement of alternative exons for the third Ig-like domain. The arrangement of these genes suggests that there are conserved mechanisms governing the expression of secreted FGF receptors as well as the expression of at least two distinct membrane-spanning forms of the FGF receptors. The diverse forms appear to be generated by alternative splicing of mRNA and selective use of polyadenylation signals.

L14 ANSWER 6 OF 6 MEDLINE DUPLICATE 3
ACCESSION NUMBER: 97229252 MEDLINE
DOCUMENT NUMBER: 97229252 PubMed ID: 9075249
TITLE: Pediatric **brain tumors** express multiple receptor tyrosine kinases including novel cell adhesion kinases.
AUTHOR: Weiner H L; Rothman M; Miller D C; Ziff E B
CORPORATE SOURCE: Department of Neurosurgery (Pediatric Neurosurgery), New York University Medical Center, NY 10016, USA.
CONTRACT NUMBER: P20 NS31088 (NINDS)
SOURCE: PEDIATRIC NEUROSURGERY, (1996 Aug) 25 (2) 64-71; discussion 71-2.
Journal code: 9114967. ISSN: 1016-2291.
PUB. COUNTRY: Switzerland
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199706
ENTRY DATE: Entered STN: 19970612
Last Updated on STN: 20000303
Entered Medline: 19970603

AB We have used the polymerase chain reaction to clone and characterize growth factor receptor tyrosine kinases (RTKs) expressed in 3 pathologically distinct pediatric **brain tumors**, an anaplastic **ependymoma**, a glioblastoma multiforme and a primitive neuroectodermal tumor (PNET). These neoplasms are presumed to be derived from embryonic neuroepithelial precursor cells of the central nervous system. This cloning demonstrated expression of 24 distinct kinase genes: 16 receptor type kinases and 8 nonreceptor type kinases. The expression of 6 receptors, including Hek2, IRR, Ryk, **FGFR3**, and 2 members of the newly identified cell adhesion kinase receptor family, DDR and TKT, in such tumors has not been reported previously. Northern analysis of mRNA levels revealed DDR expression in 6 of 7 pediatric **brain tumors** including an **ependymoma**, PNET, glioblastoma and **astrocytoma**, and also in an adult pheochromocytoma. Thus, the DDR cell adhesion kinase may be widely expressed in pediatric **brain tumors**. Also, PCR cloning may be an effective procedure for characterizing RTKs in clinical tissue samples and revealing the expression of novel RTK species.

WER 5 OF 6 MEDLINE DUPLICATE 2

ACCESSION NUMBER: 1999085118 MEDLINE
DOCUMENT NUMBER: 99085118 PubMed ID: 9864407
TITLE: Fibroblast growth factor-9 (glia-activating factor) stimulates proliferation and production of glial fibrillary acidic protein in human **gliomas** either in the presence or in the absence of the endogenous growth factor expression.
AUTHOR: Miyagi N; Kato S; Terasaki M; Aoki T; Sugita Y; Yamaguchi M; Shigemori M; Morimatsu M
CORPORATE SOURCE: Department of Pathology, Kurume University, School of Medicine, Kurume, Japan.
SOURCE: ONCOLOGY REPORTS, (1999 Jan-Feb) 6 (1) 87-92. Journal code: 9422756. ISSN: 1021-335X.
PUB. COUNTRY: Greece
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199903
ENTRY DATE: Entered STN: 19990402
Last Updated on STN: 19990402
Entered Medline: 19990322

AB We tested fibroblast growth factor-9 (FGF-9) expression in human **glioma** cells (U251MG, T98G, U87MG, KALS-1, NMC-G1) and only NMC-G1 expressed endogenous FGF-9. All cells expressed bFGF and high affinity receptors for FGFs (FGFR1 and **FGFR3**). Exogenously supplied bFGF and FGF-9 both showed mitogenic activities in all cells. Neutralizing antibody against bFGF inhibited the proliferation in U251MG and NMC-G1, however that against FGF-9 inhibited the proliferation only in NMC-G1. GFAP expression was stimulated by both FGFs in these cells. FGF-9 potentially regulates proliferation and GFAP expression in human **gliomas** either in the presence or in the absence of the endogenous growth factor expression.

L14 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:756373 CAPLUS
DOCUMENT NUMBER: 136:51990
TITLE: Expression profiling of **medulloblastoma**: PDGFRA and the RAS/MAPK pathway as therapeutic targets for metastatic disease
AUTHOR(S): MacDonald, Tobey J.; Brown, Kevin M.; LaFleur, Bonnie; Peterson, Katia; Lawlor, Christopher; Chen, Yidong; Packer, Roger J.; Cogen, Philip; Stephan, Dietrich A.
CORPORATE SOURCE: Center for Cancer and Transplantation Biology, Children's National Medical Center, Washington, DC, USA
SOURCE: Nature Genetics (2001), 29(2), 143-152
CODEN: NGENEC; ISSN: 1061-4036
PUBLISHER: Nature America Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Little is known about the genetic regulation of **medulloblastoma** dissemination, but metastatic **medulloblastoma** is highly assocd. with poor outcome. We obtained expression profiles of 23 primary **medulloblastomas** clin. designated as either metastatic (M+) or non-metastatic (M0) and identified 85 genes whose expression differed significantly between classes. Using a class prediction algorithm based on these genes and a leave-one-out approach, we assigned sample class to these tumors (M+ or M0) with 72% accuracy and to four addnl. independent tumors with 100% accuracy. We also assigned the metastatic **medulloblastoma** cell line Daoy to the metastatic class. Notably, platelet-derived growth factor receptor .alpha. (PDGFRA) and members of the downstream RAS/mitogen-activated protein kinase (MAPK) signal transduction pathway are upregulated in M+ tumors. Immunohistochem. validation on an independent set of tumors shows significant overexpression of PDGFRA in M+ tumors compared to M0 tumors. Using in vitro assays, we show that platelet-derived growth factor .alpha. (PDGFA) enhances **medulloblastoma** migration and increases downstream MAP2K1 (MEK1), MAP2K2 (MEK2), MAPK1 (p42 MAPK) and MAPK3 (p44 MAPK) phosphorylation in a dose-dependent manner. Neutralizing antibodies to PDGFRA blocks MAP2K1, MAP2K2 and MAPK1/3 phosphorylation, whereas U0126, a highly specific inhibitor of MAP2K1 and MAP2K2, also blocks MAPK1/3. Both inhibit migration and prevent PDGFA-stimulated migration. These results provide the first insight into the genetic regulation of **medulloblastoma** metastasis and are the first to suggest a role for PDGFRA and the RAS/MAPK signaling pathway in **medulloblastoma** metastasis. Inhibitors of PDGFRA and RAS proteins should therefore be considered for investigation as possible novel therapeutic strategies against **medulloblastoma**.

REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L14 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC.
ACCESSION NUMBER: 2001:265659 BIOSIS
DOCUMENT NUMBER: PREV200100265659
TITLE: Crystal structure of fibroblast growth factor 9 reveals regions implicated in dimerization and autoinhibition.
AUTHOR(S): Plotnikov, Alexander N.; Eliseenkova, Anna V.; Ibrahimi, Omar A.; Shriver, Zachary; Sasisekharan, Ram; Lemmon, Mark A.; Mohammadi, Moosa (1)
CORPORATE SOURCE: (1) Department of Pharmacology, New York University School of Medicine, New York, NY, 10016 USA
SOURCE: Journal of Biological Chemistry, (February 9, 2001) Vol. 276, No. 6, pp. 4322-4329. print.
ISSN: 0021-9258.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
AB Fibroblast growth factors (FGFs) constitute a large family of heparin-binding growth factors with diverse biological activities. FGF9 was originally described as glia-activating factor and is expressed in the nervous system as a potent mitogen for glia cells. Unlike most FGFs, FGF9 forms dimers in solution with a Kd of 680 nM. To elucidate the molecular mechanism of FGF9 dimerization, the crystal structure of FGF9 was determined at 2.2 ANG resolution. FGF9 adopts a beta-trefoil fold similar to other FGFs. However, unlike other FGFs, the N- and C-terminal regions outside the beta-trefoil core in FGF9 are ordered and involved in the formation of a 2-fold crystallographic dimer. A significant surface area (>2000 ANG2) is buried in the dimer interface that occludes a major receptor binding site of FGF9. Thus, we propose an autoinhibitory mechanism for FGF9 that is dependent on sequences outside of the beta-trefoil core. Moreover, a model is presented providing a molecular basis for the preferential affinity of FGF9 toward **FGFR3**.

L14 ANSWER 2 OF 6 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001416780 MEDLINE
DOCUMENT NUMBER: 21359863 PubMed ID: 11466624
TITLE: Frequency of **fibroblast growth factor receptor 3** mutations in sporadic tumours.
AUTHOR: Sibley K; Stern P; Knowles M A
CORPORATE SOURCE: ICRF Clinical Centre, St. James's University Hospital, Leeds, LS9 7TF, UK.
SOURCE: ONCOGENE, (2001 Jul 19) 20 (32) 4416-8. Journal code: 8711562. ISSN: 0950-9232.
PUB. COUNTRY: England: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20010813
Entered Medline: 20010809

AB Mutations in **FGFR3** have been identified in several tumour types including bladder carcinoma, cervical carcinoma, and multiple myeloma. In bladder carcinoma, we recently identified **FGFR3** mutations in 41% of tumours, making this the most frequently mutated putative oncogene identified in bladder cancer to date. We have now investigated the frequency of **FGFR3** mutation in a panel of 125 tumours and 13 cell lines from various other organs. We analysed the mutation hotspots in exons 7, 10 and 15 by direct DNA sequencing, and found one mutation in exon 7 (S249C) in 1/28 (3.5%) cervical tumours. Mutations were not detected in stomach, rectum, colon, prostate, ovarian, breast, **brain**, or renal **tumours**, nor were they found in any of the cell lines included in this study. We conclude that **FGFR3** is commonly mutated in bladder carcinoma and only rarely in cervical carcinoma. Several tumour types appear not to possess any mutations in **FGFR3**, suggesting that these mutations are important only in the development of certain types of tumour.

L20 ANSWER 3 OF 4 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 1999308632 MEDLINE
DOCUMENT NUMBER: 99308632 PubMed ID: 10380925
TITLE: Diverse signaling pathways activated by growth factor receptors induce broadly overlapping, rather than independent, sets of genes.
COMMENT: Comment in: Cell. 1999 Jun 11;97(6):675-8
AUTHOR: Fambrough D; McClure K; Kazlauskas A; **Lander E S**
CORPORATE SOURCE: Whitehead Institute for Biomedical Research, Cambridge, Massachusetts 02142, USA.
SOURCE: CELL, (1999 Jun 11) 97 (6) 727-41.
Journal code: 0413066. ISSN: 0092-8674.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199907
ENTRY DATE: Entered STN: 19990730
Last Updated on STN: 20000303
Entered Medline: 19990722

AB We sought to explore the relationship between receptor tyrosine kinase (RTK) activated signaling pathways and the transcriptional induction of immediate early genes (IEGs). Using global expression monitoring, we identified 66 fibroblast IEGs induced by platelet-derived growth factor beta receptor (PDGFRbeta) signaling. Mutant receptors lacking binding sites for activation of the PLCgamma, PI3K, SHP2, and RasGAP pathways still retain partial ability to induce 64 of these IEGs. Removal of the Grb2-binding site further broadly reduces induction. These results suggest that the diverse pathways exert broadly overlapping effects on IEG induction. Interestingly, a mutant receptor that restores the RasGAP-binding site promotes induction of an independent group of genes, normally induced by interferons. Finally, we compare the PDGFRbeta and **fibroblast growth factor receptor** 1; each induces essentially identical IEGs in fibroblasts.

L14 ANSWER 32 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2001064882 PCTFULL ED 20020822
TITLE (ENGLISH): 1983, 52881, 2398, 45449, 50289, AND 52872, G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR
TITLE (FRENCH): RECEPTEURS COUPLES A UNE PROTEINE G, NUMEROTEES 1983, 52881, 2398, 45449, 50289, ET 52872, ET UTILISATIONS CORRESPONDANTES
INVENTOR(S): GLUCKSMANN, Maria, Alexandra; GALVIN, Katherine, M.; SILOS-SANTIAGO, Inmaculada
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC.; GLUCKSMANN, Maria, Alexandra; GALVIN, Katherine, M.; SILOS-SANTIAGO, Inmaculada
DOCUMENT TYPE: Patent
PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2001064882	A2	20010907

DESIGNATED STATES: AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG

APPLICATION INFO.:	WO 2001-US6543	A	20010228
PRIORITY INFO.:	US 2000-60/186,059		20000229

DETD The subject can be a cancer patient e.g., a patient with **brain cancer**, bone **cancer**, or prostate cancer. In other embodiments, the subject is a non-human anirrial, elg., an experimental animal, e.g., an aithritic rat niodel of. . . . . is a method of evaluating a sample. The method includes providing a sample, e.g., from the subject, and determining a gene **expression profile** of the sample, wherein the profile includes a value representing the level of 1983, 52881, 2398, 45449, 50289and52872expression. ThemethodcanfLirtherincludecoiilparingthevalueo rtf-le profile (i.e., multiple values) to a reference value or reference profile. The gene **expression profile** of the sample can be obtained by any of the methods described herein 1 5 (e.g., by providing a nucleic acid. . . an indication that the subject has or is disposed to having a disorders as described herein. The method can be used to **monitor** a **treatment** for such disorders in a subject. For example, the gene **expression profile** can be determined for a sample from a subject undergoing **treatment**.

L14 ANSWER 22 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2001083781 PCTFULL ED 20020826
TITLE (ENGLISH): 14094, A NOVEL HUMAN TRYPSIN FAMILY MEMBER AND USES THEREOF
TITLE (FRENCH): 14094, UN NOUVEAU MEMBRE DANS LA FAMILLE DE LA TRYPSINE
HUMAINE ET SON UTILISATION
INVENTOR(S): MEYERS, Rachel; MACBETH, Kyle, J.
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC.; MEYERS, Rachel; MACBETH, Kyle, J.
DOCUMENT TYPE: Patent
PATENT INFORMATION:

	NUMBER	KIND	DATE
	WO 2001083781	A2	20011108
DESIGNATED STATES	AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG US UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG		
APPLICATION INFO.:	WO 2001-US13903	A	20010430
PRIORITY INFO.:	US 2000-60/200,621		20000428
	US 2000-09/633,300		20000808

DETD . . . cancerous or pre-cancerous tissue where a 14094 polypeptide or nucleic acid is expressed, e.g., breast, ovanian, colon, liver, lung, kldney, or **brain cancer**.

. . .
found in a tissue 1,vhere a 14094 polypeptide or nucieic acid is expressed, e.g., breast, ovarian, colon, liver, lung, kjdney, or **brain cancer**.

. . .
cancer is a sarcoma, a carcinoma, or an adenocarcm'oma. Preferably, the cancer is a breast, ovarian, colon, lung, liver, kidney, or **brain cancer**.

. . .
gastric cancer, esophageal cancer, rectal 5 cancer, pancreatic cancer, ovarian cancer, prostate cancer, utenne cancer, cancer of the head and neck, skin **cancer, brain cancer,** squamous cell carcinoma, sebaceous gland carcinoma.

. . .
can further inciude compar-ing the value or the profile (1.e., multiple values) to a reference value or reference profile. The gene **expression profile** of the sample can be obtained by any of the methods described herein (e.g., by providing a nuclele acid from the sample. . . is an indication that the subject has or is disposed to having a cell proliferative disorder. The method can be used to **monitor** a **treatment** for a cell protiferative disorder in a subject. For example, the gene **expression profile** can be

determined for a sample from a subject
75 -
undergoing **treatment**. The profile can be compared to a
reference profile or to a profile
obtained from the subject prior to **treatment** or prior to onset
of the disorder (see, e.g., Golub
et al. (I 999) Science 286:53 I).
. . .
context,
thc off@LjL of one cell type on another cell type in response to a
biological stimulus can be
determined, e,g., to **monitor** the effect of cell-cell
interaction at the level of gene expression,
In another embodiment, cells are contacted With a **therapeutic**
agent. The
expression profile of the celis is determined using
the array, and the **expression profile** is
compared to the profile of llke celis not contacted ivith the agent.
For
example, the assay
can be used to determine or analyze the molecular basis of an
undesirable effect of the
therapeutic agent. lf an agent is administered
therapeutically to treat one cell type but has an
undesirable effect on another cell type, the invention provides an
assay
to determine. . .

L8 ANSWER 12 OF 20 MEDLINE
ACCESSION NUMBER: 2001393249 MEDLINE
DOCUMENT NUMBER: 21064203 PubMed ID: 11122874
TITLE: Application of advances in molecular biology to the **treatment** of brain tumors.
AUTHOR: Takeshima H; Sawamura Y; Gilbert M R; Van Meir E G
CORPORATE SOURCE: Department of Neurosurgery, Faculty of Medicine, Kagoshima University, 8-35-1 Sakuraga-oka, Kagoshima 890-8520, Japan.. m2040k@khosp2.kufm.kagoshima-u.ac.jp
SOURCE: Curr Oncol Rep, (2000 Sep) 2 (5) 425-33. Ref: 56
Journal code: 100888967. ISSN: 1523-3790.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200107
ENTRY DATE: Entered STN: 20010716
Last Updated on STN: 20010716
Entered Medline: 20010712

AB Recent advances in molecular biology have substantially improved our understanding of the molecular genetics of primary brain neoplasms. Soon each histopathologic category of glioma will be further divided into subgroups according to similar genetic background, gene **expression profile**, and similarity of biologic responses to radiotherapy or chemotherapy. Identification of key molecules that are specifically altered in neoplastic cells will provide candidate molecular targets for tumor **treatment**. Novel **therapeutic** tools for targeting tumor cells, such as viral vectors for gene **therapy**, have been created. In the near future, the accumulation of new knowledge in brain tumor biology and genetics, combined with rational drug design, will revolutionize the **treatment** of malignant gliomas, which are among the most lethal human cancers.

L14 ANSWER 3 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2002059610 PCTFULL ED 20020809 EW 200231
TITLE (ENGLISH): USING OVEREXPRESSION OF LAMININ ALPHA 4 SUBUNIT AS A DIAGNOSTIC AND PROGNOSTIC INDICATOR OF MALIGNANT TUMORS
TITLE (FRENCH): UTILISATION DE LA SUREXPRESSION DE LA SOUS-UNITE DE LAMININE ALPHA 4 EN TANT QU'INDICATEUR DIAGNOSTIQUE ET PRONOSTIQUE DE TUMEURS MALIGNES
INVENTOR(S): LJUBIMOVA, Julia, Y.; LJUBIMOV, Alexander, V.; BLACK, Keith, L.
PATENT ASSIGNEE(S): CEDARS-SINAI MEDICAL CENTER
AGENT: STEINBERG, Nisan, A., Ph.D.
LANGUAGE OF FILING: English
LANGUAGE OF PUBL.: English
DOCUMENT TYPE: Patent
PATENT INFORMATION:

NUMBER	KIND	DATE
WO 2002059610	A2	20020801

DESIGNATED STATES AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ PH PL PT RO RU SD SE SG SI SK SL TJ TM TR TT TZ UA UG UZ VN YU ZA ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GW ML MR NE SN TD TG
APPLICATION INFO.: WO 2001-US50292 A 20011219
PRIORITY INFO.: US 2000-09/741,550 20001219
ABEN Disclosed is a method of diagnosing the presence of a malignant tumor, including a glioma, in a human subject, which involves detecting overexpression of laminin *4 subunit protein or laminin *4-specific mRNA, compared to the expression level in a normal tissue control. Also disclosed are a method of predicting the recurrence of a malignant tumor in a human subject from whom a malignant tumor has been resected and a method of classifying the grade of a malignant tumor, such as a glial tumor, based on a molecular classification.

ABFR L'invention concerne un procede de diagnostic de la presence de tumeurs malignes, y compris de gliomes, chez l'homme, qui implique la detection de la surexpression de la proteine de sous-unite de laminine α4 ou d'un ARNm specifique de la laminine α4, par comparaison avec le niveau d'expression dans un temoin tissulaire normal. L'invention concerne egalement un procede permettant de prevoir la recurrence d'une tumeur maligne chez un homme ayant subi une resection de tumeur maligne, ainsi qu'un procede de determination de la classe d'une tumeur maligne, telle qu'une tumeur gliale, sur la base d'une classification moleculaire.

L14 ANSWER 4 OF 33 PCTFULL COPYRIGHT 2003 Univentio
ACCESSION NUMBER: 2002057457 PCTFULL ED 20020801 EW 200230
TITLE (ENGLISH): 55562 AND 21617, NOVEL HUMAN PROTEINS AND METHODS OF USE THEREOF
TITLE (FRENCH): 55562 ET 21617, NOUVELLES PROTEINES HUMAINES ET LEURS METHODES D'UTILISATION
INVENTOR(S): MEYERS, Rachel, A.; BANDARU, Rajasekhar
PATENT ASSIGNEE(S): MILLENNIUM PHARMACEUTICALS, INC., for all designates States except US; MEYERS, Rachel, A., for US only; BANDARU, Rajasekhar, for US only
AGENT: COLLAZO, Diana, M.
LANGUAGE OF FILING: English
LANGUAGE OF PUBL.: English
DOCUMENT TYPE: Patent
PATENT INFORMATION:

	NUMBER	KIND	DATE
	WO 2002057457	A2	20020725
DESIGNATED STATES	AE AG AL AM AT AU AZ BA BB BG BR BY BZ CA CH CN CO CR CU CZ DE DK DM DZ EC EE ES FI GB GD GE GH GM HR HU ID IL IN IS JP KE KG KP KR KZ LC LK LR LS LT LU LV MA MD MG MK MN MW MX MZ NO NZ OM PH PL PT RO RU SD SE SG SI SK SL TJ TM TN TR TT TZ UA UG US UZ VN YU ZA ZM ZW GH GM KE LS MW MZ SD SL SZ TZ UG ZM ZW AM AZ BY KG KZ MD RU TJ TM AT BE CH CY DE DK ES FI FR GB GR IE IT LU MC NL PT SE TR BF BJ CF CG CI CM GA GN GQ GW ML MR NE SN TD TG		
APPLICATION INFO.:	WO 2001-US49416	A	20011218
PRIORITY INFO.:	US 2000-60/256,249		20001218
	US 2000-60/256,405		20001218

ABEN The invention provides isolated nucleic acids molecules, designated 21617 and 55562 nucleic acid molecules, which encode novel dehydrogenase or tetratricopeptide repeat members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing 21617 or 55562 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 21617 or 55562 gene has been introduced or disrupted.

The invention still further provides isolated 21617 or 55562 proteins, fusion proteins, antigenic peptides and anti-21617 or 55562 antibodies. Diagnostics methods utilizing compositions of the invention are also provided.

ABFR La presente invention concerne des molecules d'acides nucleiques isolees, designees sous le nom de molecules d'acides nucleiques 21617 et 55562, codant de nouvelles repetitions de la deshydrogenase ou du tetratrichopeptide. L'invention concerne egalement des molecules d'acides nucleiques antisens, des vecteurs d'expression recombines contenant ces molecules d'acides nucleiques 21617 ou 55562, des cellules hotes dans lesquelles ces vecteurs d'expression ont ete introduits et des animaux transgeniques non humains dans lesquels le gene 21617 ou 55562 a ete introduit ou interrompu. L'invention concerne egalement des proteines 21617 ou 55562 isolees, des proteines hybrides, des peptides antigeniques et des anticorps anti-21617 ou 55562. L'invention concerne egalement des methodes diagnostiques utilisant des compositions de la

présente invention.

L2 ANSWER 11 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 2000:49185 SCISEARCH
THE GENUINE ARTICLE: 273BX
TITLE: Cell-type specific expression in the pituitary: physiology and gene therapy
AUTHOR: Castro M G (Reprint); Windeatt S; SmithArica J; Lowenstein P R
CORPORATE SOURCE: UNIV MANCHESTER, SCH MED, MOL MED UNIT, ROOM I-302, OXFORD RD, MANCHESTER M13 9PT, LANCS, ENGLAND (Reprint)
COUNTRY OF AUTHOR: ENGLAND
SOURCE: BIOCHEMICAL SOCIETY TRANSACTIONS, (**DEC 1999**) Vol. 27, Part 6, pp. 858-863.
Publisher: PORTLAND PRESS, 59 PORTLAND PLACE, LONDON W1N 3AJ, ENGLAND.
ISSN: 0300-5127.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 49

L2 ANSWER 18 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 1998:946863 SCISEARCH
THE GENUINE ARTICLE: 146TR
TITLE: The cytogenesis and pathogenesis of pituitary adenomas
AUTHOR: Asa S L (Reprint); Ezzat S
CORPORATE SOURCE: MT SINAI HOSP, DEPT PATHOL & LAB MED, 600 UNIV AVE, TORONTO, ON M5G 1X5, CANADA (Reprint); MT SINAI HOSP, DEPT MED, TORONTO, ON M5G 1X5, CANADA; UNIV TORONTO, DEPT LAB MED & PATHOBIOL, TORONTO, ON M5G 1X5, CANADA; UNIV TORONTO, DEPT MED, TORONTO, ON M5G 1X5, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: ENDOCRINE REVIEWS, (**DEC 1998**) Vol. 19, No. 6, pp. 798-827.
Publisher: ENDOCRINE SOC, 4350 EAST WEST HIGHWAY SUITE 500, BETHESDA, MD 20814-4110.
ISSN: 0163-769X.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 361

L2 ANSWER 16 OF 23 SCISEARCH COPYRIGHT 2003 ISI (R)
ACCESSION NUMBER: 1999:271844 SCISEARCH
THE GENUINE ARTICLE: 182EY
TITLE: The pathology of pituitary tumors
AUTHOR: Asa S L (Reprint)
CORPORATE SOURCE: MT SINAI HOSP, DEPT PATHOL & LAB MED, 600 UNIV AVE, TORONTO, ON M5G 1X5, CANADA (Reprint); UNIV TORONTO, DEPT LAB MED & PATHOBIOL, TORONTO, ON, CANADA
COUNTRY OF AUTHOR: CANADA
SOURCE: ENDOCRINOLOGY AND METABOLISM CLINICS OF NORTH AMERICA, (**MAR 1999**) Vol. 28, No. 1, pp. 13-&.
Publisher: W B SAUNDERS CO, INDEPENDENCE SQUARE WEST CURTIS CENTER, STE 300, PHILADELPHIA, PA 19106-3399.
ISSN: 0889-8529.
DOCUMENT TYPE: General Review; Journal
FILE SEGMENT: LIFE; CLIN
LANGUAGE: English
REFERENCE COUNT: 153

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The pathologist plays an important role in the distinction of pituitary adenomas from other tumors and tumor-like lesions of the sellar region, and in the accurate morphologic characterization of pitutiary adenomas. A clinicopathologic classification of pituitary adenomas is based on cell differentiation correlated with clinical evidence of hormone secretion; this classification emphasizes clinically relevant features that can offer guidance for patient management. The application of a rational approach to the immunohistochemical analysis of these lesions can be used to evaluate pathogenetic and prognostic markers and to predict responses to specific therapeutic modalities.